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(54) Title: POLYNUCLEOTIDES, POLYPEPTIDES EXPRESSED BY THE POLYNUCLEOTIDES AND METHODS FOR THEIR USE

(57) Abstract: Novel polynucleotides including partial and extended sequences, and open reading frames, are provided, together with probes and primers, DNA constructs comprising the polynucleotides, biological materials and organisms incorporating the polynucleotides, polypeptides expressed by the polynucleotides, and methods for using the polynucleotides and polypeptides.

**POLYNUCLEOTIDES, POLYPEPTIDES EXPRESSED BY THE  
POLYNUCLEOTIDES AND METHODS FOR THEIR USE**

5    Technical Field of the Invention

This invention relates to polynucleotides believed to be novel, including partial, extended and full length sequences, as well as probes and primers, genetic constructs comprising the polynucleotides, biological materials incorporating the polynucleotides, polypeptides expressed by the polynucleotides, and methods for 10 using the polynucleotides and polypeptides.

15    Background of the Invention

Sequencing of the genomes, or portions of the genomes, of numerous biological materials, including humans, animals, microorganisms and various 15 plant varieties, has been and is being carried out on a large scale. Polynucleotides identified using sequencing techniques may be partial or full-length genes, and may contain open reading frames, or portions of open reading frames, that encode polypeptides. Putative polypeptides may be determined based on polynucleotide sequences. The sequencing data relating to polynucleotides thus represents 20 valuable and useful information.

Polynucleotides may be analyzed for various degrees of novelty by comparing identified sequences to sequences published in various public domain databases, such as EMBL. Newly identified polynucleotides and putative 25 polypeptides may also be compared to polynucleotides and polypeptides contained in public domain information to ascertain homology to known polynucleotides and polypeptides. In this way, the degree of similarity, identity or homology of polynucleotides and polypeptides of unknown function may be determined relative to polynucleotides and polypeptides having known functions.

Information relating to the sequences of isolated polynucleotides may be 30 used in a variety of ways. Specified polynucleotides having a particular sequence may be isolated, or synthesized, for use in *in vivo* or *in vitro* experimentation as

probes or primers. Alternatively, collections of sequences of isolated polynucleotides may be stored using magnetic or optical storage medium, and analyzed or manipulated using computer hardware and software, as well as other types of tools.

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Summary of the Invention

The present invention relates to polynucleotide sequences identified in the attached Sequence Listing as SEQ ID NOS: 1-35, variants of those sequences, extended sequences comprising the sequences set out in SEQ ID NOS: 1-35 and their variants, probes and primers corresponding to the sequences set out in SEQ ID NOS: 1-35 and their variants, polynucleotides comprising at least a specified number of contiguous residues of any of the polynucleotides identified as SEQ ID NOS: 1-35 (*x*-mers), and extended sequences comprising portions of the sequences set out in SEQ ID NOS: 1-35, all of which are referred to herein, 10 collectively, as "polynucleotides of the present invention." 15

The polynucleotide sequences identified as SEQ ID NOS: 1-35 were derived from mammalian sources, namely, from mouse airways induced eosinophilia, rat dermal papilla and mouse stromal cells. Some of the polynucleotides of the present invention are "partial" sequences, in that they do 20 not represent a full-length gene encoding a full-length polypeptide. Such partial sequences may be extended by further analyzing and sequencing the EST clones from which the sequences were obtained, or by analyzing and sequencing various DNA libraries (e.g. cDNA or genomic) using primers and/or probes and well known hybridization and/or PCR techniques. The partial sequences identified as 25 SEQ ID NOS: 1-35 may thus be extended until an open reading frame encoding a polypeptide, a full-length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full-length polynucleotides and genes, are described as "corresponding to" a sequence identified as one of the sequences of SEQ ID NOS: 30 1-35 or a variant thereof, or a portion of one of the sequences of SEQ ID NOS: 1-35 or a variant thereof, when the extended polynucleotide comprises an identified

sequence or its variant, or an identified contiguous portion (x-mer) of one of the sequences of SEQ ID NOS: 1-35 or a variant thereof.

The polynucleotides identified as SEQ ID NOS: 1-35 were isolated from mouse and rat cDNA clones and represent sequences that are expressed in the tissue from which the cDNA was prepared. The sequence information may be used to isolate or synthesize expressible DNA molecules, such as open reading frames or full-length genes, that can then be used as expressible or otherwise functional DNA in transgenic mammals and other organisms. Similarly, RNA sequences, reverse sequences, complementary sequences, anti-sense sequences and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NOS: 1-35.

In a first aspect, the present invention provides isolated polynucleotide sequences comprising a polynucleotide selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-35; (b) complements of the sequences recited in SEQ ID NO: 1-35; (c) reverse complements of the sequences recited in SEQ ID NO: 1-35; (d) reverse sequences of the sequences recited in SEQ ID NO: 1-35; (e) sequences having either 40%, 60%, 75% or 90% identical nucleotides, as defined herein, to a sequence of (a) – (d); probes and primers corresponding to the sequences set out in SEQ ID NO: 1-35; polynucleotides comprising at least a specified number of contiguous residues of any of the polynucleotides identified as SEQ ID NO: 1-35; and extended sequences comprising portions of the sequences set out in SEQ ID NO: 1-35; all of which are referred to herein as "polynucleotides of the present invention". The present invention also provides isolated polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 36-65; polypeptide variants of those sequences; and polypeptides comprising the isolated polypeptide sequences and variants of those sequences.

In another aspect, the present invention provides genetic constructs comprising a polynucleotide of the present invention, either alone, or in combination with one or more additional polynucleotides of the present invention,

or in combination with one or more known polynucleotides, together with cells and target organisms comprising such constructs.

The polynucleotides identified as SEQ ID NOS: 1-35 may contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides.

5 Additionally, open reading frames encoding polypeptides may be identified in extended or full-length sequences corresponding to the sequences set out as SEQ ID NOS: 1-35. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification

10 based on codon frequencies, etc. Suitable tools and software for ORF analysis are available, for example, on the Internet at <http://www.ncbi.nlm.nih.gov/gorf/gorf.html>. Open reading frames and portions of open reading frames may be identified in the polynucleotides of the present invention. Once a partial open reading frame is identified, the polynucleotide may

15 be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified. Thus, polynucleotides and open reading frames encoding polypeptides may be identified using the polynucleotides of the present invention.

Once open reading frames are identified in the polynucleotides of the present invention, the open reading frames may be isolated and/or synthesized.

20 Expressible DNA constructs may then be constructed that comprise the open reading frames and suitable promoters, initiators, terminators, etc., which are well known in the art. Such DNA constructs may be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells

25 may include various prokaryotic and eukaryotic cells.

Polypeptides encoded by the polynucleotides of the present invention may be expressed and used in various assays to determine their biological activity. Such polypeptides may be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of

30 interacting proteins or other compounds.

In another aspect, the present invention provides isolated polypeptides encoded, or partially encoded, by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full-length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide that comprises an isolated polynucleotide sequence or variant provided herein. Polypeptides of the present invention may be naturally purified products, or may be produced partially or wholly using recombinant techniques. Such polypeptides may be glycosylated with bacterial, fungal, mammalian or other eukaryotic carbohydrates or may be non-glycosylated. In specific embodiments, the inventive polypeptides comprise 10 an amino acid sequence selected from the group consisting of SEQ ID NO: 36-65.

Polypeptides of the present invention may be produced recombinantly by inserting a polynucleotide sequence that encodes the polypeptide into a genetic construct and expressing the polypeptide in an appropriate host. Any of a variety 15 of genetic constructs known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with a genetic construct containing a polynucleotide that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are 20 *Escherichia coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The polynucleotide sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

25 In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence encoded by a polynucleotide of the present invention. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule 30 that is capable of binding one or more reactants. The active site may be made up

of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity.

Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the 5 polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using, for example, the representative assays provided below.

10 Portions and other variants of the inventive polypeptides may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the 15 commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2154, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems, Inc. (Foster City, California), and may 20 be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed, site-specific mutagenesis (Kunkel, *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985). Sections of polynucleotide sequence may also be removed using standard techniques to permit preparation of truncated 25 polypeptides.

In general, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure. In certain embodiments, described in detail below, the isolated polypeptides 30 are incorporated into pharmaceutical compositions or vaccines.

The present invention also contemplates methods for modulating the polynucleotide and/or polypeptide content and composition of an organism, such methods involving stably incorporating into the genome of the organism a construct containing DNA of the present invention. In one embodiment, the target 5 organism is a mammal, preferably a human, for example for human gene therapy. In a related aspect, a method for producing an organism having an altered genotype or phenotype is provided, the method comprising transforming a cell with a DNA construct of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and 10 mature organism growth.

The isolated polynucleotides of the present invention have utility in genome mapping, in physical mapping, and in positional cloning of genes. Additionally, the polynucleotide sequences identified as SEQ ID NOS: 1-35 and their variants may be used to design oligonucleotide probes and primers. 15 Oligonucleotide probes and primers have sequences that are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. Oligonucleotide probes designed using the polynucleotides of the present invention may be used to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA 20 sequences in their cells using techniques that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the polynucleotides of the present invention may also be used in connection with various microarray 25 technologies, including the microarray technology of Affymetrix (Santa Clara, CA).

The polynucleotides of the present invention may also be used to tag or identify an organism or reproductive material therefrom. Such tagging may be accomplished, for example, by stably introducing a non-disruptive non-functional 30 heterologous polynucleotide identifier into an organism, the polynucleotide comprising one of the polynucleotides of the present invention.

Detailed Description

Polynucleotides were isolated by high throughput sequencing of cDNA libraries prepared from mouse airway-induced eosinophilia, rat dermal papilla and mouse stromal cells as described below, in Example 1. Isolated polynucleotides of the present invention include the polynucleotides identified as SEQ ID NOS: 1-35; isolated polynucleotides comprising a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 1-35; isolated polynucleotides comprising at least a specified number of contiguous residues (*x*-mers) of any of the polynucleotides identified as SEQ ID NOS: 1-35; polynucleotides complementary to any of the above polynucleotides; anti-sense sequences corresponding to any of the above polynucleotides; and variants of any of the above polynucleotides, as that term is described in this specification. The present invention also provides isolated polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 36-65; polypeptide variants of those sequences; and polypeptides comprising the isolated polypeptide sequences and variants of those sequences.

The correspondence of isolated polynucleotides encoding isolated polypeptides of the present invention, and the functionality of the polypeptides, are shown, below, in Table 1.

20

Table 1

SEQ ID NO Polynucleotides	SEQ ID NO Polypeptides	Activity Category	Functionality
1	36	Secretory molecule	Hypothetical 131.1 kDa protein
2	37	Secretory molecule/cytokine/ cell signaling	ZCYTO7 belongs to a family of IL-17-related cytokines differing in patterns of expression and proinflammatory responses that may be transduced through a cognate set of cell surface receptors. IL-17 is a T cell-derived cytokine that may play an important role in the initiation or maintenance of the proinflammatory response. Whereas expression of IL-17 is restricted to activated T cells, the IL-17 receptor is found to be

			widely expressed, a finding consistent with the pleiotropic activities of IL-17.
3	38	Secretory molecule	Novel
4	39	Receptor/cytokine/ cell signaling	Tumor endothelial marker 1 precursor
5	40	Secretory molecule	ERO1-L (ERO1-like protein) is involved in oxidative endoplasmic reticulum (ER) protein folding in mammalian cells. Oxidizing conditions must be maintained in the ER to allow the formation of disulfide bonds in secretory proteins. A family of conserved genes, termed ERO for ER oxidoreductins, plays a key role in this process. ERO1-L is a type II integral membrane protein.
6	41	Secretory molecule	Novel
7	42	Receptor/transcriptio n factor	EMR2 is an EGF-like module that is part of the epidermal growth factor (EGF)-TM7 proteins, which also include EMR1, (EGF-like molecule containing mucin-like hormone receptor 1) F4/80, and CD97. These proteins constitute a recently defined class B GPCR subfamily and are predominantly expressed on leukocytes. These molecules possess N-terminal EGF-like domains coupled to a seven-span transmembrane (7TM) moiety via a mucin-like spacer domain. EMR2 contains a total of five tandem EGF-like domains and expresses similar protein isoforms consisting of various numbers of EGF-like domains as a result of alternative RNA splicing. EMR2 share many characteristics with CD97, including highly homologous EGF-like domains and identical gene organization, indicating that both genes are the products of a recent gene duplication event. Both EMR2 and CD97 are highly expressed in immune tissues; however, unlike

			CD97, which is ubiquitously expressed in most cell types, EMR2 expression is restricted to monocytes, macrophages
8	43	Secretory molecule/ cell structure/motility, extracellular matrix	Bone/cartilage proteoglycan I (BGN) is also known as biglycan or PG-S1. BGN is found in the extracellular matrices of several connective tissues, especially in articular cartilages. The two glycosaminoglycan chains attached to BGN can be either chondroitin sulfate or dermatan sulfate. BGN belongs to the small interstitial proteoglycans family. BGN is a small leucine-rich proteoglycan and is a nonfibrillar extracellular matrix component with functions that include the positive regulation of bone formation. It is synthesized as a precursor with an NH(2)-terminal propeptide that is cleaved to yield the mature form found in vertebrate tissues. Bone morphogenetic protein-1 (BMP-1) cleaves proBGN at a single site, removing the propeptide and producing BGN. Soluble BGN purified from rat thymic myoid cells had hemopoietic activity capable of inducing preferential growth and differentiation of monocytic lineage cells from various hemopoietic sources, including brain microglial cells. The haemopoietic BGN plays an important role in generating brain-specific circumstances for development of microglial/monocytic cells
9	44	Secretory molecule	Tubulointerstitial nephritis antigen (TIN-ag) is a basement membrane glycoprotein reactive with autoantibodies in some forms of immunologically mediated human tubulointerstitial nephritis. TIN1 and TIN2 are alternatively spliced products of the TIN-Ag gene. The

			open reading frames of TIN1 and TIN2 indicates the presence of a signal peptide and putative pre-propeptide and both forms contain putative calcium-binding sites. TIN1 additionally contains a characteristic laminin-like epidermal growth factor (EGF) motif and significant homology within the carboxy terminus with the cysteine proteinase family of enzymes. The EGF motif bears important similarities in the positions of cysteines with two motifs in the propeptide of von Willebrand factor. The EGF motif and part of the region that is homologous with the cysteine proteinase family are removed from the TIN2 cDNA. The rest of the TIN1 and TIN2 sequences are identical. TIN-ag is expressed mainly in the kidney and in the intestinal epithelium.
10		Receptor-like molecule	Novel
11	45	Secretory molecule/gene/protein expression, RNA synthesis, transcription factors	Toso is a cell surface, specific regulator of Fas-induced apoptosis in T cells. Fas is a surface receptor that can transmit signals for apoptosis. Toso is expressed in lymphoid cells and expression is enhanced after cell-specific activation processes in T cells. Toso appeared limited to inhibition of apoptosis mediated by members of the TNF receptor family and was capable of inhibiting T cell self-killing induced by TCR activation processes that up-regulate Fas ligand. Toso inhibits caspase-8 processing, the most upstream caspase activity in Fas-mediated signaling, potentially through activation of cFLIP. Toso therefore serves as a novel regulator of Fas-mediated apoptosis and may act as a regulator of cell fate in T cells and

			<u>other hematopoietic lineages.</u>
12	46	Secretory molecule/gene/protein expression, RNA synthesis, transcription factors	Surface glycoprotein CD59 is a phosphatidyl-inositol-glycan-anchored glycoprotein involved in T-cell activation and restriction of complement-mediated lysis. It is also known as protectin, and is ubiquitously expressed on benign and malignant cells. CD59 inhibits complement (C)-mediated lysis of target cells by preventing the formation of the membrane attack complex, in the terminal step of C-activation. Recent experimental evidence demonstrates that CD59 is the main restriction factor of C-mediated lysis of malignant cells of different histotypes. Additionally, a soluble form of CD59, that retains its anchoring ability and functional properties, has been identified in body fluids and in culture supernatants of different malignant cells. CD59 may protect neoplastic cells from C-mediated lysis, contributing to their escape from innate C-control and to tumor progression. The expression of CD59 by neoplastic cells may contribute to impair the therapeutic efficacy of C-activating monoclonal antibodies (mAb) directed to tumor-associated antigens. CD59 can be utilized to improve the therapeutic efficacy of clinical approaches of humoral immunotherapy with C-activating mAb in human malignancies.
13	47	Secretory molecules/cell or organism defense, homeostasis, detoxification	Cytochrome B561 (cyb561) is a secretory vesicle-specific electron transport protein unique to neuroendocrine secretory vesicles. It binds two heme groups non-covalently and is an integral membrane protein. It acts as an electron channel and mediates

			equilibration of ascorbate-semidehydroascorbate inside the secretory vesicle with the ascorbate redox pair in the cytoplasm. The role for this function is to regenerate ascorbate inside the secretory vesicle for use by monooxygenases. The secretory vesicles contain catecholamines and amidated peptides. Cyb561 belongs to the eukaryotic b561 family.
14	48	Secretory molecule	Novel
15	49	Receptor-like molecule/ gene or protein expression, RNA synthesis, transcription factor	High affinity immunoglobulin epsilon receptor beta-subunit (FCER1) is also known as IgE Fc receptor, beta-subunit, FCER1b or FCE1b. FCER1 binds to the Fc region of immunoglobulins epsilon and is a high affinity receptor. FCER1 plays a role in initiating the allergic response where binding of allergen to receptor-bound IgE leads to cell activation and the release of mediators, such as histamine. FCER1 is responsible for the manifestations of allergy and induces the secretion of important lymphokines. It functions as a tetramer consisting of an alpha chain, a beta chain, and two disulfide-linked gamma chains and is an integral membrane protein. Variants of the FCER1B gene have been identified, which are associated with an increased risk of developing atopy and bronchial asthma. Atopic dermatitis is a common skin disease frequently associated with allergic disorders such as allergic rhinitis and asthma.
16	50	Receptor-like molecule	Hypothetical 10.3 kDa protein
17	51	Secretory molecule/antigen processing	Lysosomal thiol reductase IP30 catalyzes disulfide bond reduction both <i>in vitro</i> and <i>in vivo</i> and is optimally active at acidic pH. IP30

			is important in disulfide bond reduction of proteins delivered to MHC class II-containing compartments and consequently in antigen processing. IP30 can be mediated by multiple lysosomal proteases. Proteins internalized into the endocytic pathway are usually degraded. Efficient proteolysis requires denaturation, induced by acidic conditions within lysosomes, and reduction of inter- and intrachain disulfide bonds. The active site, determined by mutagenesis, consists of a pair of cysteine residues separated by two amino acids, similar to other enzymes of the thioredoxin family.
18		Receptor-like molecule	RNA binding protein.
19	52	Secretory molecule/cellular	Notch4-like protein (ZNEU1) is part of the NOTCH4 family that encodes receptors responsible for cell fate decisions during development. These Notch receptors and their ligands, Delta and Jagged, have been implicated in several diseases. When truncated, constitutively active mutant forms of the Notch receptor appear to be involved in T-cell leukemia, mammary carcinomas and a tumorous germline phenotype. Notch4 genes are expressed specifically in endothelial cells.
20	53	Secretory molecule	Novel
21	54	Secretory molecule/transporter	Serotransferrin (siderophilin) (Tf) or beta-1-metal binding globulin is part of the transferrin family. Transferrins are iron binding transport proteins which can bind two atoms of ferric iron in association with the binding of an anion, usually bicarbonate. Tf is responsible for the transport of iron from sites of absorption and heme degradation to those of storage and

			utilization. Serum transferrin also has a further role in stimulating cell proliferation. Tf gene expression is modulated by vitamin A, testosterone, and peptide hormones.
22	55	Secretory molecule/gene or protein expression, RNA synthesis, transcription factor	Insulin-like growth factor binding protein 5 protease (IGFBP-5) modulates the effects of insulin growth factors (IGFs) on cells. IGFBP-5 is synthesized by smooth muscle cells and binds to the extracellular matrix. It is also secreted into conditioned medium of cultured cells and is cleaved into fragments by a concomitantly produced protease. These fragments have reduced affinity for the IGFs. IGFBP-5 protease belongs to a family of serine-metallo proteases.
23	56	Secretory molecule/cellular development	Major epididymis-specific protein E4 is also known as epididymal protein BE-20. It belongs to WAP-type 'four-disulfide core' family and plays a role in the maturation of spermatozoa during its movement through the epididymis and the capacity of sperm to fertilize ova. Expression of E4 was located to the epithelial cells of the cauda epididymis and proximal segment of the ductus deferens by <i>in situ</i> hybridization. No expression was found in sections of the corpus and caput epididymis, testis, and liver.
24		Secretory molecule/cell signaling	TNFR-related death receptor-6 DR6 contains an extracellular region containing varying numbers of cysteine-rich domains and an intracellular region that contains the death domain. Death receptors are activated in a ligand-dependent or independent manner and transduce apoptotic signals via their respective intracellular death domains.
25	57	Receptor-like molecule	Novel

26	58	Secretory molecule/regulation	Channel inducing factor precursor (CHIF) or corticosteroid-induced protein induces a potassium channel when expressed in <i>Xenopus</i> oocytes and activates endogenous oocyte transport proteins. It is a type I membrane protein selectively present in the distal parts of the nephron (medullary and papillary collecting ducts and end portions of cortical collecting tubule) and in the epithelial cells of the distal colon. No expression is found in renal proximal tubule, loop of Henle and distal tubule, proximal colon, small intestine, lung, choroid plexus, salivary glands, or brain. CHIF belongs to the ATP1G1 /PLM / Mat-8 family and exhibits significant homologies with proteins that are putatively regulatory (phospholemman, gamma-subunit of Na(+)-K(+)-ATPase, Mat-8).
27	59	Secretory molecule	Hepatocellular carcinoma-associated antigen 112.
28	60	Receptor-like molecule/homeostasis	Lymphatic endothelium-specific hyaluronan receptor LYVE-1 is a major receptor for hyaluronan (HA) on the lymph vessel wall molecule that binds both soluble and immobilized HA. LYVE-1 plays a role in the control of the HA pathway. The extracellular matrix glycosaminoglycan hyaluronan (HA) is an abundant component of skin and mesenchymal tissues where it facilitates cell migration during wound healing, inflammation, and embryonic morphogenesis. Both during normal tissue homeostasis and particularly after tissue injury, HA is mobilized from these sites through lymphatic vessels to the lymph nodes where it is degraded before entering the circulation for rapid uptake by the liver. LYVE-1 is similar to the

			CD44 HA receptor, but in contrast to CD44, LYVE-1 colocalizes with HA on the luminal face of the lymph vessel wall and is completely absent from blood vessels.
29	61	Receptor-like molecule/cell signaling	G protein-coupled receptor GPR35 is an integral membrane protein that belongs to family 1 of G-protein coupled receptors (GPCR). The GPCR family shares a structural motif of seven transmembrane segments with large numbers of conserved residues in those regions.
30	62	Receptor-like molecule	Tumor-associated glycoprotein E4 is also known as Taal or Tage4 and belongs to the immunoglobulin superfamily. This family contains cell adhesion molecules which have wide-ranging functions and mediate a variety of homotypic and heterotypic cellular interactions playing a general role in cell surface recognition. The Tage4 gene product is closely related to the hepatocellular carcinoma antigen TuAg.1. Tage4 is a glycoprotein expressed at the surface of colon carcinoma cell lines, but at a very low level in normal adult colon and lung tissue and not in normal tissues tested.
31	63	Secretory molecule	Hypothetical 28.6 kDa protein is also known as plunc, for palate, lung, and nasal epithelium clone. Expression of plunc is associated with the palate, nasal septum, and nasal conchae. It is also expressed strongly in the trachea and bronchi of the adult lung. No significant homologies with known genes were observed at the nucleotide level and limited amino acid homology with two salivary gland-specific proteins was noted. The amino acid sequence revealed consensus sequences for N-glycosylation, protein kinase C and

			casein kinase phosphorylation, as well as a leucine zipper. In addition, an unique amino acid sequence repeat sequence is located near the amino-terminal portion of the protein.
32	64	Secretory molecule	Claudin-18 (Cldn18) is a component of tight junction (TJ) strands and belongs to the claudin family. Claudins are integral membrane protein component of tight junctions, a structure controlling cell-to-cell adhesion and, consequently, regulating paracellular and transcellular transport of solutes across epithelia and endothelia. The claudin family also includes occludin and 17 other distinct claudins. Claudin family members are tetraspan transmembrane proteins that are localized in cell-specific TJs. In multicellular organisms, various compositionally distinct fluid compartments are established by epithelial and endothelial cellular sheets. For these cells to function as barriers, TJs are considered to create a primary barrier for the diffusion of solutes through the paracellular pathway. Claudins are therefore responsible for TJ-specific obliteration of the intercellular space.
33		Secretory molecule	Glutamine repeat protein 1 (GRP-1) contains simple tandem repeats of the trinucleotide sequence CAG that encode homopolymeric stretches of glutamine. Although polyglutamine has been identified in diverse proteins, it is present predominantly in transcription factors. Greater than two-thirds of GRP-1 are only two amino acids, namely glutamine (50%) and histidine (18%). There are four polyglutamine motifs interspersed with histidine-rich regions. There is also a putative

			nuclear localization signal flanked by sites for possible serine phosphorylation. GRP-1 mRNA was expressed constitutively in some macrophage cell lines and B and T cell lines. Interferon-gamma or lipopolysaccharide augmented GRP-1 mRNA expression in the mouse macrophage cell line ANA-1. Because polyglutamine motifs can cause protein oligomerization and can function as transcriptional activation domains, GRP-1 is a transcription factor associated with interferon-gamma- or lipopolysaccharide-induced activation of macrophages.
34		Secretory molecule	Alpha-1 collagen
35	65	Receptor-like molecule/Cell signaling	Gdnf family receptor alpha 4, transmembrane isoform (Gfra4) is a members of the Gdnf protein family that signal through receptors consisting of a GPI-linked GFRalpha subunit and the transmembrane tyrosine kinase Ret. Gfra4 is expressed in many tissues, including nervous system, in which intron retention leads to a putative intracellular or secreted GFRalpha4 protein. Efficient splicing occurs only in thyroid, parathyroid, and pituitary and less in adrenal glands. A splice form that leads to a GPI-linked GFRalpha4 receptor is expressed in juvenile thyroid and parathyroid glands. In newborn and mature thyroid as well as in parathyroid and pituitary glands major transcripts encode for a putative transmembrane isoform of GFRalpha4. GFRalpha4 expression may restrict the inherited cancer syndrome multiple endocrine neoplasia type 2, associated with mutations in RET, to these cells.

The word "polynucleotide(s)," as used herein, means a polymeric collection of nucleotides and includes DNA and corresponding RNA molecules and both single and double stranded molecules, including HnRNA and mRNA molecules, sense and anti-sense strands of DNA and RNA molecules, and 5 comprehends cDNA, genomic DNA, and wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and "corresponds to" a DNA molecule in a generally one-to-one manner. An mRNA molecule "corresponds to" an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide of the present invention may be an entire gene, or 10 any portion thereof. A gene is a DNA sequence which codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well 15 known in the art and are described, for example, in Robinson-Benion *et al.*, *Methods in Enzymol.* 254(23): 363-375, 1995 and Kawasaki *et al.*, *Artific. Organs* 20 (8): 836-848, 1996.

Identification of genomic DNA and heterologous species DNA can be accomplished by standard DNA/DNA hybridization techniques, under 20 appropriately stringent conditions, using all or part of a cDNA sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and/or protein sequences can be used to amplify and identify genomic and cDNA sequences. Synthetic DNA corresponding to the identified sequences and variants 25 may be produced by conventional synthesis methods. All of the polynucleotides described herein are isolated and purified, as those terms are commonly used in the art.

As used herein, the term "oligonucleotide" refers to a relatively short segment of a polynucleotide sequence, generally comprising between 6 and 60 30 nucleotides, and comprehends both probes for use in hybridization assays and primers for use in the amplification of DNA by polymerase chain reaction.

As used herein, the term “*x*-mer,” with reference to a specific value of “*x*,” refers to a polynucleotide comprising at least a specified number (“*x*”) of contiguous residues of any of the polynucleotides identified as SEQ ID NOS: 1-35. The value of *x* may be from about 20 to about 600, depending upon the 5 specific sequence.

As used herein, the term “polypeptide” encompasses amino acid chains of any length, including full-length proteins, wherein amino acid residues are linked by covalent peptide bonds. Polypeptides of the present invention may be naturally purified products, or may be produced partially or wholly using 10 recombinant techniques. Such polypeptides may be glycosylated with mammalian or other eukaryotic carbohydrates or may be non-glycosylated.

According to one embodiment, “variants” of the polynucleotides of the present invention, including the polynucleotides set forth as SEQ ID NOS: 1-35, as that term is used herein, comprehends polynucleotides producing an “E” value 15 of 0.01 or less, as described below, or having at least a specified percentage identity to a polynucleotide of the present invention, as described below. Polynucleotide variants of the present invention may be naturally occurring allelic variants, or non-naturally occurring variants.

Polynucleotide and polypeptide sequences may be aligned, and 20 percentages of identical residues in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. Polynucleotides may also be analyzed using the BLASTX algorithm, which 25 compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. The percentage identity of polypeptide sequences may be examined using the BLASTP algorithm. The BLASTN, BLASTP and BLASTX algorithms are available on the NCBI anonymous FTP server (<ftp://ncbi.nlm.nih.gov>) under /blast/executables/ and are 30 available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894,

USA. The BLASTN algorithm Version 2.0.11 [Jan-20-2000], set to the parameters described below, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm, set to the parameters described below, is preferred for use in the 5 determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX, is described at NCBI's website at URL <http://www.ncbi.nlm.nih.gov/BLAST/newblast.html> and in the publication of Altschul, *et al.*, *Nucleic Acids Res.* 25: 3389-3402, 1997.

10 The FASTA and FASTX algorithms are available on the Internet at the ftp site <ftp://ftp.virginia.edu/pub/>, and from the University of Virginia by contacting David Hudson, Vice Provost for Research, University of Virginia, P.O. Box 9025, Charlottesville, VA 22906-9025, USA. The FASTA algorithm, set to the default parameters described in the documentation and distributed with the algorithm, 15 may be used in the determination of polynucleotide variants. The readme files for FASTA and FASTX Version 1.0x that are distributed with the algorithms describe the use of the algorithms and describe the default parameters. The use of the FASTA and FASTX algorithms is described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson, *Methods in Enzymol.* 20 183:63-98, 1990. The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity: Unix running command with default parameter values thus: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results; the Parameters are : -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File 25 Out] Optional.

30

The "hits" to one or more database sequences by a queried sequence produced by BLASTN or FASTA or a similar algorithm align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally 5 represent an overlap over only a fraction of the sequence length of the queried sequence.

The BLASTN and FASTA algorithms produce "Expect" values for alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a 10 database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database, such as the preferred EMBL database, indicates true similarity. For example, an E value of 0.1 assigned to a hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a 15 similar score simply by chance. The aligned and matched portions of the sequences, then, have a probability of 90% of being the same by this criterion. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN or FASTA algorithm.

According to one embodiment, "variant" polynucleotides, with reference 20 to each of the polynucleotides of the present invention, preferably comprise sequences having the same number or fewer nucleic acids than each of the polynucleotides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide of the present invention. That is, a variant 25 polynucleotide is any sequence that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or FASTA algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of 30 the present invention that has at least a 99% probability of being the same as the

polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or FASTA algorithms set at the default parameters.

Alternatively, variant polynucleotides of the present invention may comprise a sequence exhibiting at least about 40%, more preferably at least about 5 60%, more preferably yet at least about 75%, and most preferably at least about 90% similarity to a polynucleotide of the present invention, determined as described below. The percentage similarity is determined by aligning sequences using one of the BLASTN or FASTA algorithms, set at default parameters, and identifying the number of identical nucleic acids over the best aligned portion; 10 dividing the number of identical nucleic acids by the total number of nucleic acids of the polynucleotide of the present invention; and then multiplying by 100 to determine the percentage similarity. For example, a polynucleotide of the present invention having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the 15 alignment produced by the BLASTN algorithm using the default parameters. The 23 nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage similarity of the polynucleotide of the present invention to the hit in the EMBL library is thus 21/220 times 100, or 9.5%. The polynucleotide sequence in the EMBL database is thus not a variant of a 20 polynucleotide of the present invention.

Alternatively, variant polynucleotides of the present invention hybridize to a polynucleotide of the present invention under stringent hybridization conditions. As used herein, "stringent conditions" mean prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two 25 washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses allelic variants of the disclosed sequences, together with DNA sequences that differ from the disclosed sequences but which, due to the degeneracy of the genetic code, encode a polypeptide which 30 is the same as that encoded by a DNA sequence disclosed herein. Thus, polynucleotides comprising sequences that differ from the polynucleotide

sequences recited in SEQ ID NOS: 1-35, or complements, reverse sequences, or reverse complements of those sequences as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide 5 sequences recited in SEQ ID NOS: 1-35, or complements, reverse complements, or reverse sequences as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention.

The polynucleotides of the present invention may be isolated from various 10 DNA libraries, or may be synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (e.g. Beckman Oligo 1000M DNA Synthesizer) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA- 15 manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5-nucleotide overhang. The next segment may 20 then be synthesized in a similar fashion, with a 5-nucleotide overhang on the opposite strand. The "sticky" ends ensure proper ligation when the two portions are hybridized. In this way, a complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

SEQ ID NOS: 2, 3, 5, 7-9, 11, 12, 14, 15, 17, 19-21, 23, 26, 28 and 30-32 25 are full-length sequences. The remaining polynucleotides are referred to as "partial" sequences, in that they may not represent the full coding portion of a gene encoding a naturally occurring polypeptide. The partial polynucleotide sequences disclosed herein may be employed to obtain the corresponding full-length genes for various species and organisms by, for example, screening DNA 30 expression libraries using hybridization probes based on the polynucleotides of the present invention, or using PCR amplification with primers based upon the

polynucleotides of the present invention. In this way one can, using methods well known in the art, extend a polynucleotide of the present invention upstream and downstream of the corresponding mRNA, as well as identify the corresponding genomic DNA, including the promoter and enhancer regions, of the complete gene. The present invention thus comprehends isolated polynucleotides comprising a sequence identified in SEQ ID NOS: 1-35, or a variant of one of the specified sequences, that encode a functional polypeptide, including full-length genes. Such extended polynucleotides may have a length of from about 50 to about 4,000 nucleic acids or base pairs, and preferably have a length of less than about 4,000 nucleic acids or base pairs, more preferably yet a length of less than about 3,000 nucleic acids or base pairs, more preferably yet a length of less than about 2,000 nucleic acids or base pairs. Under some circumstances, extended polynucleotides of the present invention may have a length of less than about 1,800 nucleic acids or base pairs, preferably less than about 1,600 nucleic acids or base pairs, more preferably less than about 1,400 nucleic acids or base pairs, more preferably yet less than about 1,200 nucleic acids or base pairs, and most preferably less than about 1,000 nucleic acids or base pairs.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues ( $x$ -mers) of any of the polynucleotides identified as SEQ ID NOS: 1-35 or their variants. According to preferred embodiments, the value of  $x$  is preferably at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer a 250-mer, or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide identified as SEQ ID NOS: 1-35 or a variant of one of the polynucleotides identified as SEQ ID NOS: 1-35.

Polynucleotide probes and primers complementary to and/or corresponding to SEQ ID NOS: 1-35, and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest. An

oligonucleotide probe or primer is described as "corresponding to" a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NOS: 1-35 or a variant, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NOS: 1-35 or a variant of one of the specified sequences.

Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared using, for example, the BLAST algorithm as described above, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a second DNA strand under stringent hybridization conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM and preferably less than about 200 mM. Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C and most preferably greater than about 37°C. Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as probe composition, presence of organic solvents and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone. The DNA from plants or samples or products containing plant material can be either genomic DNA or DNA derived by preparing cDNA from the RNA present in the sample.

In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the case of DNA-RNA hybridization, the mRNA from expressed genes would then be detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the case of RNA-RNA hybridization, RNA probes could be used. In addition, artificial analogs of DNA hybridizing specifically to target sequences could also be employed.

In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and 5 primers of the present invention may be from about 8 to 100 base pairs in length or, preferably from about 10 to 50 base pairs in length or, more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, potential for formation of loops 10 and other factors, which are well known in the art. Tools and software suitable for designing probes, and especially suitable for designing PCR primers, are available on the Internet, for example, URL <http://www.horizonpress.com/pcr/>. Preferred techniques for designing PCR primers are also disclosed in Dieffenbach and Dyksler, *PCR primer: a laboratory manual*. Cold Spring Harbor Laboratory 15 Press, Cold Spring Harbor, NY, 1995.

A plurality of oligonucleotide probes or primers corresponding to a polynucleotide of the present invention may be provided in a kit form. Such kits generally comprise multiple DNA or oligonucleotide probes, each probe being specific for a polynucleotide sequence. Kits of the present invention may 20 comprise one or more probes or primers corresponding to a polynucleotide of the present invention, including a polynucleotide sequence identified in SEQ ID NOS: 1-35.

In one embodiment useful for high-throughput assays, the oligonucleotide probe kits of the present invention comprise multiple probes in an array format, 25 wherein each probe is immobilized in a predefined, spatially addressable location on the surface of a solid substrate. Array formats which may be usefully employed in the present invention are disclosed, for example, in U.S. Patents No. 5,412,087, 5,545,531, and PCT Publication No. WO 95/00530, the disclosures of which are hereby incorporated by reference.

30 Oligonucleotide probes for use in the present invention may be constructed synthetically prior to immobilization on an array, using techniques well known in

the art (see, for example, *Oligonucleotide Synthesis: A Practical Approach*, Gait, ed., IRL Press, Oxford, 1984). Automated equipment for the synthesis of oligonucleotides is available commercially from such companies as Perkin Elmer/Applied Biosystems Division (Foster City, CA) and may be operated 5 according to the manufacturer's instructions. Alternatively, the probes may be constructed directly on the surface of the array using techniques taught, for example, in PCT Publication No. WO 95/00530.

The solid substrate and the surface thereof preferably form a rigid support and are generally formed from the same material. Examples of materials from 10 which the solid substrate may be constructed include polymers, plastics, resins, membranes, polysaccharides, silica or silica-based materials, carbon, metals and inorganic glasses. Synthetically prepared probes may be immobilized on the surface of the solid substrate using techniques well known in the art, such as those disclosed in U.S. Patent No. 5,412,087.

15 In one such technique, compounds having protected functional groups, such as thiols protected with photochemically removable protecting groups, are attached to the surface of the substrate. Selected regions of the surface are then irradiated with a light source, preferably a laser, to provide reactive thiol groups. This irradiation step is generally performed using a mask having apertures at 20 predefined locations using photolithographic techniques well known in the art of semiconductors. The reactive thiol groups are then incubated with the oligonucleotide probe to be immobilized. The precise conditions for incubation, such as temperature, time and pH, depend on the specific probe and can be easily determined by one of skill in the art. The surface of the substrate is washed free of 25 unbound probe and the irradiation step is repeated using a second mask having a different pattern of apertures. The surface is subsequently incubated with a second, different, probe. Each oligonucleotide probe is typically immobilized in a discrete area of less than about 1 mm<sup>2</sup>. Preferably each discrete area is less than about 10,000 mm<sup>2</sup>, more preferably less than about 100 mm<sup>2</sup>. In this manner, a 30 multitude of oligonucleotide probes may be immobilized at predefined locations on the array.

The resulting array may be employed to screen for differences in organisms or samples or products containing genetic material as follows. Genomic or cDNA libraries are prepared using techniques well known in the art. The resulting target DNA is then labeled with a suitable marker, such as a 5 radiolabel, chromophore, fluorophore or chemiluminescent agent, using protocols well known for those skilled in the art. A solution of the labeled target DNA is contacted with the surface of the array and incubated for a suitable period of time.

The surface of the array is then washed free of unbound target DNA and the probes to which the target DNA hybridized are determined by identifying 10 those regions of the array to which the markers are attached. When the marker is a radiolabel, such as  $^{32}\text{P}$ , autoradiography is employed as the detection method. In one embodiment, the marker is a fluorophore, such as fluorescein, and the location of bound target DNA is determined by means of fluorescence spectroscopy. Automated equipment for use in fluorescence scanning of oligonucleotide probe 15 arrays is available from Affymetrix, Inc. (Santa Clara, CA) and may be operated according to the manufacturer's instructions. Such equipment may be employed to determine the intensity of fluorescence at each predefined location on the array, thereby providing a measure of the amount of target DNA bound at each location. Such an assay would be able to indicate not only the absence and presence of the 20 marker probe in the target, but also the quantitative amount as well.

In this manner, oligonucleotide probe kits of the present invention may be employed to examine the presence/absence (or relative amounts in case of mixtures) of polynucleotides in different samples or products containing different materials rapidly and in a cost-effective manner.

25 Another aspect of the present invention involves collections of a plurality of polynucleotides of the present invention. A collection of a plurality of the polynucleotides of the present invention, particularly the polynucleotides identified as SEQ ID NOS: 1-35, may be recorded and/or stored on a storage medium and subsequently accessed for purposes of analysis, comparison, etc. 30 One utility for such sets of sequences is the analysis of the set, either alone or together with other sequences sets, for single nucleotide polymorphisms (SNPs)

between sequences from different tissues and/or individuals for genetic studies, mapping and fingerprinting purposes. Suitable storage media include magnetic media such as magnetic diskettes, magnetic tapes, CD-ROM storage media, optical storage media, and the like. Suitable storage media and methods for 5 recording and storing information, as well as accessing information such as polynucleotide sequences recorded on such media, are well known in the art. The polynucleotide information stored on the storage medium is preferably computer-readable and may be used for analysis and comparison of the polynucleotide information.

10 Another aspect of the present invention thus involves storage medium on which are recorded a collection of the polynucleotides of the present invention, particularly a collection of the polynucleotides identified as SEQ ID NOS: 1-35. According to one embodiment, the storage medium includes a collection of at least 20, preferably at least 50, more preferably at least 100, and most preferably 15 at least 200 of the polynucleotides of the present invention, preferably the polynucleotides identified as SEQ ID NOS: 1-35, or variants of those polynucleotides.

Another aspect of the present invention involves a combination of polynucleotides, the combination containing at least 5, preferably at least 10, more 20 preferably at least 20, and most preferably at least 50 different polynucleotides of the present invention, including polynucleotides selected from SEQ ID NOS: 1-35, or variants of these polynucleotides.

In another aspect, the present invention provides DNA constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading 25 frame coding for at least a functional portion of a polypeptide encoded by a polynucleotide of the present invention; and a gene termination sequence. The open reading frame may be orientated in either a sense or antisense direction. DNA constructs comprising a non-coding region of a gene coding for an enzyme 30 encoded by the above DNA sequences or a nucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Preferably, the gene promoter and

termination sequences are functional in a host cell. More preferably, the gene promoter and termination sequences are common to those of the polynucleotide being introduced. Other promoter and termination sequences generally used in the art, such as the Cauliflower Mosaic Virus (CMV) promoter, with or without 5 enhancers, such as the Kozak sequence or Omega enhancer, and *Agrobacterium tumefaciens* nopaline synthase terminator may be usefully employed in the present invention. Tissue-specific promoters may be employed in order to target expression to one or more desired tissues. The DNA construct may further include a marker for the identification of transformed cells.

10 Techniques for operatively linking the components of the DNA constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, *Molecular Cloning: a laboratory manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. The DNA constructs of the present invention 15 may be linked to a vector having at least one replication system, for example, *Escherichia coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced and the correctness of the manipulation determined.

Transgenic cells comprising the DNA constructs of the present invention are provided, together with organisms comprising such transgenic cells.  
20 Techniques for stably incorporating DNA constructs into the genome of target organisms, such as mammals, are well known in the art and include electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of technique will depend upon the target organism to be transformed. In 25 one embodiment, naked DNA is injected or delivered orally. Once the cells are transformed, cells having the DNA construct incorporated in their genome are selected. Transgenic cells may then be cultured in an appropriate medium, using techniques well known in the art.

In yet a further aspect, the present invention provides methods for 30 modifying the level (concentration) or activity of a polypeptide in a host organism, comprising stably incorporating into the genome of the organism a

DNA construct of the present invention. The DNA constructs of the present invention may be used to transform a variety of organisms, including mammals, for example to make experimental gene knock out or transgenic animals.

Further, the polynucleotides of the present invention have particular application for use as non-disruptive tags for marking organisms, including commercially valuable animals, fish, bacteria and yeasts. DNA constructs comprising polynucleotides of the present invention may be stably introduced into an organism as heterologous, non-functional, non-disruptive tags. It is then possible to identify the origin or source of the organism at a later date by determining the presence or absence of the tag(s) in a sample of material.

Detection of the tag(s) may be accomplished using a variety of conventional techniques, and will generally involve the use of nucleic acid probes. Sensitivity in assaying the presence of probe can be usefully increased by using branched oligonucleotides, as described by Horn *et al.*, *Nucleic Acids Res.* 15 25(23):4842-4849, 1997, enabling to detect as few as 50 DNA molecules in the sample.

In particular, the polynucleotides of the present invention encode polypeptides that have important roles in processes such as induction of growth, differentiation of tissue-specific cells, cell migration, cell proliferation, and cell-cell interaction. These polypeptides are important in the maintenance of tissue integrity, and thus are important in processes such as wound healing. Some of these polypeptides act as modulators of immune responses, such as immunologically active polypeptides for the benefit of offspring. In addition, many polypeptides are immunologically active, making them important therapeutic targets in a whole range of disease states. Antibodies to the polypeptides of the present invention and small molecule inhibitors related to the polypeptides of the present invention may also be used for modulating immune responses and for treatment of diseases according to the present invention.

SEQ ID NOS: 1; 2; 4; 5; 6; 8; 9; 11; 12; 14; 17; 19-24; 26; 27; 31-34  
30 encode secreted polypeptides. SEQ ID NOS: 10; 15; 16; 18; 25; 28; 30; and 35  
encode polypeptides acting as receptors. SEQ ID NOS: 2; 4; 24; 29 and 35

encode polypeptides with cell signaling activity, which may be either intracellular or extracellular. Kinase genes, for example, encode polypeptides that phosphorylate specific substrates during cell-to-cell signaling. While some kinases are involved in normal metabolism and nucleotide production, others are 5 significant for altering the activity of many cellular processes through the phosphorylation of specific proteins. Polypeptides encoded by these genes are important in the transmission of intracellular signals resulting from the binding of extracellular ligands such as hormones, growth factors or cytokines to membrane-bound receptors. The utility of polynucleotides encoding kinases resides in the 10 manipulation of their signaling activities and downstream effects for the diagnosis and treatment of mammalian diseases that may be a consequence of inappropriate expression of these kinase genes.

SEQ ID NOS: 2 and 4 encode polypeptides with cytokine activity. Cytokine or growth factor polynucleotides encode polypeptides involved in 15 intercellular signaling and represent another important class of molecules. Polynucleotides encoding such genes have utility in the diagnosis and treatment of disease.

SEQ ID NOS: 7; 11; 12; 15 and 22 encode polypeptides with transcription factor activity. These polynucleotides encode polypeptides required for the control 20 of synthesis of proteins in tissue specific manner and have utility for the modification of protein synthesis for the control of disease.

SEQ ID NOS: 8 encode polypeptides acting in the extracellular matrix.

SEQ ID NOS: 11; 12; 15 and 22 encode polypeptides with RNA synthesis activities.

SEQ ID NO: 12 encodes a polypeptide having CD antigen activity. Such polynucleotides have utility as modulators of the composition, expression level and class of CD antigen expressed, which influence immune responses to self-antigens, neo-antigens and infectious agents.

Further exemplary specific utilities, for exemplary polynucleotides of the 30 present invention, are specified in the Table below.

SEQ ID NO:	UTILITY
2	Promoting immune response as part of a vaccine or anti-cancer treatment. Inhibitors of this molecule can be useful as anti-inflammatory treatment, e.g. for autoimmune diseases or allergies.
11; 19	Utility as a target for cancer treatment and as an immunoregulatory and anti-inflammatory molecule
12	Diagnostic for specific types of cancer and for development of an anti-cancer treatment.
15	As a target for antagonists in the treatment of diseases such as asthma and allergy.
22	Useful to inhibit or enhance the activity of the soluble molecule that binds this protein.
28	Useful to promote or block cell trafficking and therefore in the treatment as anti-inflammatory and/or vaccine adjuvant where it can promoter inflammation.
35	Useful for tissue and neural regeneration.

The following examples are offered by way of illustration and not by way of limitation.

5

#### Example 1

##### ISOLATION OF cDNA SEQUENCES FROM MAMMALIAN EXPRESSION LIBRARIES

The cDNA sequences of the present invention were obtained by high-throughput sequencing of cDNA expression libraries constructed mouse airways-induced eosinophilia, rat dermal papilla and mouse stromal cells. The cDNA libraries were prepared as follows.

##### *cDNA Library from Dermal Papilla (DEPA)*

Dermal papilla cells from rat hair vibrissae (whiskers) were grown in culture and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's

specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

5     *cDNA library from mouse airway-induced eosinophilia (MALA)*

Airway eosinophilia were induced in BALB/cByJ mice by administering 2 µg ovalbumin in 2 mg alum adjuvant intraperitoneally on day 0 and day 14, and subsequently 100 µg ovalbumin in 50 µl phosphate buffered saline (PBS) intranasally route on day 28. The accumulated eosinophils in the lungs were 10 detected by washing the airways of the anesthetized mice with saline, collecting the washings (bronchoalveolar lavage or BAL), and counting the numbers of eosinophils. The mice were sacrificed and total RNA was isolated from whole lung tissue using TRIzol Reagent (BRL Life Technologies). mRNA was isolated by using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), 15 according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

*cDNA Expression Library from Peripheral Lymph Node Stromal Cells (MLSA)*

20     The peripheral axillary and brachial lymph nodes of BALB/cByJ mice with the flaky skin (*fsn*) mutation (Jackson Laboratories, Bar Harbour, MN) were dissected out. Single cell suspensions were obtained from the lymph nodes and cultured in tissue culture flasks at  $10^7$  cells /ml in 20% fetal calf serum and Dulbecco's Minimum Essential Medium. After 2 days the non-adherent cells were 25 removed. The adherent cells were cultured for a further 2 days and then treated with 0.25 g/100ml Trypsin (ICN, Aurora, OH) and re-cultured. After a further 4 days, non-adherent cells were discarded and adherent cells removed by trypsinization. Remaining adherent cells were physically removed by scraping with a rubber policeman. All adherent stromal cells were pooled.

*cDNA Expression Library from Flaky skin lymph node stromal cells in pBK-CMV  
(MLSA)*

Stromal cells from Flaky skin mice lymph nodes were grown in culture and the total RNA extracted from these cells using established protocols. Total 5 RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit 10 (Stratagene).

cDNA sequences were obtained by high-throughput sequencing of the cDNA libraries described above using a Prism 377 sequencer (Perkin Elmer/Applied Biosystems Division, Foster City CA), and are provided in SEQ ID NO: 1-35, with corresponding polypeptide sequences in SEQ ID NOS: 36-65.

15

#### EXAMPLE 2

Analysis of cDNA sequences using BLAST algorithms

BLASTN Polynucleotide analysis

20 The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithm BLASTN. Comparisons of DNA sequences provided in SEQ ID NOS: 1-35, to sequences in the EMBL DNA database (using BLASTN) were made as of November, 2000, using Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p blastn -d embldb -e 10 -G0 -E0 -r 1 -v 30 -b 30 -i queryseq -o.

25 The sequences of SEQ ID NOS: 1, 3, 4, 6-11, 13, 18, 21, 22, 24, 25, 28-  
30, 33 and 34 were determined to have less than 50% identity, determined as described above, to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NOS: 2, 12, 30 14-16, 20 and 35 were determined to have less than 75% identity, determined as described above, to sequences in the EMBL database using the computer

algorithm BLASTN, as described above. The sequences of SEQ ID NOS: 17, 19, 23 and 27 were determined to have less than 90% identity, determined as described above, to sequences in the EMBL database using the computer algorithm BLASTN, as described above. Finally, the sequences of SEQ ID NOS: 5, 26 and 32 were determined to have less than 98% identity, determined as described above, to sequences in the EMBL database using the computer algorithm BLASTN, as described above.

#### BLASTP Polypeptide analysis

10 The sequences of SEQ ID NOS: 37, 41, 42, 44, 46-50, 55, 56 and 59 were determined to have less than 50% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 36, 38, 43, 45 and 60 were determined to have less than 75% identity, determined as described above, to 15 sequences in the SwissProt database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 39, 54 and 58 were determined to have less than 90% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. Finally, the sequences of SEQ ID NOS: 53, 57, 62 and 65 were determined to 20 have less than 98% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTP, as described above.

#### BLASTX Polynucleotide Analysis

The sequences of SEQ ID NOS: 2-4, 6-16, 18, 22-24, 26-30 and 33-35 25 were determined to have less than 50% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NOS: 1, 19, 20, 25 and 32 were determined to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as 30 described above. Finally, the sequences of SEQ ID NOS: 5, 17, 21 and 31 were determined to have less than 90% identity, determined as described above, to

sequences in the SwissProt database using the computer algorithm BLASTX, as described above.

5

### Example 2

#### ISOLATION AND CHARACTERIZATION OF THE HUMAN HOMOLOG OF MUKS1

This example demonstrates that an isolated cDNA may be used to isolate its homologue from a different species, the corresponding polypeptide may be expressed and the function of the polypeptide can be determined, starting the whole process from an isolated cDNA obtained as described above.

Analysis of RNA transcripts by Northern Blotting

Northern analysis to determine the size and distribution of mRNA for the clone muKS1 (SEQ ID NO: 66; isolated from a mouse keratinocyte stem cell cDNA library using high-throughput sequencing as described above) was performed by probing murine tissue mRNA blots with a probe consisting of nucleotides 268-499 of muKS1, radioactively labeled with [ $\alpha^{32}\text{P}$ ]-dCTP. Prehybridization, hybridization, washing and probe labeling were performed as described in Sambrook *et al.*, *Ibid.* mRNA for muKS1 was 1.6 kb in size and was observed to be most abundant in brain, lung, muscle and heart. Expression could also be detected in lower intestine, skin and kidney. No detectable signal was found in testis, spleen, liver, thymus and stomach.

25 *Human homologue of muKS1*

MuKS1 (SEQ ID NO: 66) was used to search the EMBL database (Release 50 plus updates to June, 1998) to identify human EST homologues. The top three homologies were to the following ESTs: accession numbers AA643952, HS1301003 and AA865643. These showed 92.63% identity over 285 nucleotides, 93.64% over 283 nucleotides and 94.035% over 285 nucleotides, respectively. Frame shifts were identified in AA643952 and HS1301003 when

translated. Combination of all three ESTs identified the human homologue huKS1 (SEQ ID NO: 67) and translated polypeptide SEQ ID NO: 67. Alignment of muKS1 and huKS1 polypeptides indicated 95% identity over 96 amino acids.

5 *Bacterial expression and purification of muKS1 and huKS1*

Polynucleotides 269-502 of muKS1 (SEQ ID NO: 69), encoding amino acids 23-99 of polypeptide muKS1 (SEQ ID NO: 70), and polynucleotides 55-288 of huKS1 (SEQ ID NO: 71), encoding amino acids 19-95 of polypeptide huKS1 (SEQ ID NO: 72), were cloned into the bacterial expression vector pET-16b 10 (Novagen, Madison, WI), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent *E. coli* BL21(DE3) (Novagen) as described in Sambrook *et al.*, *Ibid*.

Starter cultures of recombinant *E. coli* BL21(DE3) (Novagen) transformed with bacterial expression vector pET16b containing SEQ ID NO: 69 (muKS1a) 15 and SEQ ID NO: 71 (huKS1a) were grown in NZY broth containing 100 µg/ml ampicillin (Gibco-BRL Life Technologies) at 37°C. Cultures were spun down and used to inoculate 800 ml of NZY broth and 100 µg/ml ampicillin. Cultures were grown until the OD<sub>595</sub> of the cells was between 0.4 and 0.8. Bacterial expression was induced for 3 hours with 1 mM IPTG. Bacterial expression produced an 20 induced band of approximately 15 kDa for muKS1a and huKS1a.

MuKS1a and huKS1a were expressed in insoluble inclusion bodies. In order to purify the polypeptides, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM β-Mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP-40 was added and the mix incubated on ice for 10 minutes. 25 Lysates were further disrupted by sonication on ice at 95 W for 4 x 15 seconds and then centrifuged for 10 minutes at 18,000 rpm to pellet the inclusion bodies.

The pellet containing the inclusion bodies was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14,000 rpm for 15 minutes at 4°C and the 30 supernatant discarded. The pellet was once more re-suspended in lysis buffer

containing 0.5% w/v CHAPS, sonicated, centrifuged and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M guanidine HCl, 0.5 M NaCl, 20 mM Tris-HCl pH 8.0), sonicated at 95 W for 4 x 15 sec and centrifuged for 10 minutes at 18,000 rpm and 4°C to remove debris. The 5 supernatant was stored at 4°C. MuKS1a and huKS1a were purified by virtue of the N-terminal 6x histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's protocol. Proteins were purified twice over the column to reduce endotoxin contamination. In order to re-fold the 10 proteins once purified, the protein solution was dialysed in a 4 M-2 M urea gradient in 20 mM Tris-HCl pH 7.5 containing 10% glycerol overnight at 4°C. The protein was then further dialysed 2x against 2 litres of 20 mM Tris-HCl pH 7.5 containing 10% glycerol.

15 *Injection of bacterially expressed muKS1a into nude mice*

Two nude mice were anaesthetised intraperitoneally with 75 µl of 1/10 dilution of Hypnorm (Janssen Pharmaceuticals, Buckinghamshire, England) in phosphate buffered saline. 20 µg of bacterially expressed muKS1a (SEQ ID NO: 20 70) was injected subcutaneously in the left hind foot, ear and left hand side of the back. The same volume of phosphate buffered saline was injected in the same sites but on the right hand side of the same animal. Mice were left for 18 hours and then examined for inflammation. Both mice showed a red swelling in the ear 25 and foot sites injected with the bacterially expressed protein. No obvious inflammation could be identified in either back site. Mice were culled and biopsies taken from the ear, back and foot sites and fixed in 3.7% formol saline. Biopsies were embedded, sectioned and stained with Haemotoxylin and eosin. Sites injected with muKS1a had a marked increase in polymorphonuclear 30 granulocytes, whereas sites injected with phosphate buffered saline had a low background infiltrate of polymorphonuclear granulocytes.

Chemokines are a large superfamily of highly basic secreted proteins with a broad number of functions (Baggiolini *et al.*, *Annu. Rev. Immunol.* 15:675-705, 1997; Ward *et al.*, *Immunity* 9:1-11, 1998; Horuk, *Nature* 393:524-525, 1998). The polypeptide sequences of muKS1 and huKS1 have similarity to CXC chemokines, suggesting that this protein will act like other CXC chemokines. The *in vivo* data from nude mice supports this hypothesis. This chemokine-like protein may therefore be expected to stimulate leukocyte, epithelial, stromal and neuronal cell migration, promote angiogenesis and vascular development, promote neuronal patterning, hematopoietic stem cell mobilization, keratinocyte and epithelial stem cell patterning and development, activation and proliferation of leukocytes, and promotion of migration in wound healing events. It has recently been shown that receptors to chemokines act as co-receptors for HIV-1 infection of CD4+ cells (Cairns *et al.*, *Nature Medicine* 4:563-568, 1998) and that high circulating levels of chemokines can render a degree of immunity to those exposed to the HIV virus (Zagury *et al.*, *Proc. Natl. Acad. Sci. USA* 95:3857-3861, 1998). This novel gene and its encoded protein may thus be usefully employed as regulators of epithelial, lymphoid, myeloid, stromal and neuronal cells migration and cancers; as agents for the treatment of cancers, neuro-degenerative diseases, inflammatory autoimmune diseases such as psoriasis, asthma and Crohns disease; for use in wound healing; and as agents for the prevention of HIV-1 binding and infection of leukocytes.

SEQ ID NOS: 1-72 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties.

While in the foregoing specification this invention has been described in relation to certain preferred embodiments, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details

described herein may be varied considerably without departing from the basic principles of the invention.

We claim:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of: (1) sequences recited in SEQ ID NOS: 1-35; (2) complements of the sequences recited in SEQ ID NOS: 1-35; (3) reverse complements of the sequences recited in SEQ ID NOS: 1-35; (4) reverse sequences of the sequences recited in SEQ ID NOS: 1-35 (5) sequences having at least a 99% probability of being the same as a sequence recited in (1) – (4) above as determined using computer algorithm BLASTN; (6) sequences having at least 50% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (7) sequences having at least 75% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (8) sequences having at least 90% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (9) sequences having at least 95% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (10) nucleotide sequences that hybridize to a sequence recited in (1) – (4) above under stringent hybridization conditions; (11) nucleotide sequences that are 200-mers of a sequence recited in (1) – (4) above; (12) nucleotide sequences that are 100-mers of a sequence recited in (1) – (4) above; (13) nucleotide sequences that are 40-mers of a sequence recited in (1) – (4) above; (14) nucleotide sequences that are 20-mers of a sequence recited in (1) – (4) above; and (15) nucleotide sequences that are degeneratively equivalent to a sequence recited in (1) – (4) above.
2. An oligonucleotide comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in claim 1.
3. A genetic construct comprising an isolated polynucleotide of claim 1.

4. A host cell transformed with a genetic construct of claim 3.

5. An isolated polypeptide encoded by a polynucleotide of claim 1.

5 6. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 36-65; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP; (c) sequences having at least 50% identity to a sequence provided in  
10 SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP; (d) sequences having at least 75% identity to a sequence provided in SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP; (e) sequences having at least 90% identity to a sequence provided in SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP; and (f) sequences having at  
15 least 95% identity to a sequence provided in SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP.

7. An isolated polynucleotide encoding a polypeptide of claim 6.

20 8. An isolated polypeptide comprising at least a functional portion of a polypeptide comprising an amino acid sequence selected from the group consisting of: (a) sequences provided in SEQ ID NOS: 36-65; (b) sequences having at least a 99% probability of being the same as a sequence of SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP; (c) sequences  
25 having at least 50% identity to a sequence provided in SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP; (d) sequences having at least 75% identity to a sequence provided in SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP; (e) sequences having at least 90% identity to a sequence provided in SEQ ID NOS: 36-65, as determined using the computer  
30 algorithm BLASTP and (f) sequences having at least 95% identity to a sequence

provided in SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP.

9. A composition comprising a polypeptide according to any one of  
5. claims 6 and 8 and at least one component selected from the group consisting of:  
physiologically acceptable carriers and immunostimulants.

10. A composition comprising a polynucleotide according to claim 1  
and at least one component selected from the group consisting of  
10 pharmaceutically acceptable carriers and immunostimulants.

11. A method for treating a disorder in a mammal comprising  
administering a composition according to claim 9.

15 12. A method for treating a disorder in a mammal comprising  
administering a composition according to claim 10.

13. A diagnostic kit comprising at least one oligonucleotide according  
to claim 2.

20 14. An organism comprising a host cell according to claim 4.

**SEQUENCE LISTING**

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&lt;211&gt; 2494

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&lt;213&gt; Mouse

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&lt;211&gt; 2305

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&lt;213&gt; Mouse

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&lt;211&gt; 881

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 25

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&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 26

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&lt;210&gt; 27

&lt;211&gt; 750

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 27

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<212> DNA  
<213> Mouse

<210> 29  
<211> 1854  
<212> DNA  
<213> Mouse

<400> 29

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&lt;210&gt; 30

&lt;211&gt; 2866

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 30

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&lt;210&gt; 31

&lt;211&gt; 1093

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 31

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&lt;210&gt; 32

&lt;211&gt; 1353

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 32

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&lt;210&gt; 33

&lt;211&gt; 1046

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 33

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&lt;210&gt; 34

&lt;211&gt; 1261

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 34

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a						1261

&lt;210&gt; 35

&lt;211&gt; 995

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 35

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atgtgcactg	agaaaaaaaaaa	aaaaaaaaaa	aaaaaa			995

&lt;210&gt; 36

&lt;211&gt; 747

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 36

Glu Ala Thr Val Ile Thr Thr Glu Lys Arg Glu Arg Pro Ala Pro Pro

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Arg Glu Leu Leu Val Pro Gln Ala Glu Val Thr Ala Arg Ser			Leu Arg
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Leu Gln Trp Val Pro Gly Ser Asp Gly Ala Ser Pro Ile Arg Tyr Phe			
35	40	45	
Thr Val Gln Val Arg Glu Leu Pro Gly Gly Glu Trp Gln Thr Tyr Ser			
50	55	60	
Ser Ser Ile Ser His Glu Ala Thr Leu Cys Ala Val Glu Arg Leu Arg			
65	70	75	80
Pro Phe Thr Ser Tyr Lys Leu Arg Leu Lys Ala Thr Asn Asp Ile Gly			
85	90	95	
Asp Ser Asp Phe Ser Ala Glu Thr Glu Ala Val Thr Thr Leu Gln Asp			
100	105	110	
Val Pro Gly Glu Pro Pro Gly Ser Val Ser Ala Thr Pro His Thr Thr			
115	120	125	
Ser Ser Val Leu Ile Gln Trp Gln Pro Pro Arg Asp Glu Ser Leu Asn			
130	135	140	
Gly Leu Leu Gln Gly Tyr Arg Ile Tyr Tyr Arg Glu Leu Glu Ser Glu			
145	150	155	160
Thr Gly Leu Ser Pro Glu Pro Lys Thr Leu Lys Ser Pro Ser Ala Leu			
165	170	175	
Arg Ala Glu Leu Thr Ala Gln Ser Ser Phe Lys Thr Val Asn Ser Ser			
180	185	190	
Ser Thr Leu Thr Thr Tyr Glu Leu Thr His Leu Lys Lys Tyr Arg Arg			
195	200	205	
Tyr Glu Val Ile Met Thr Ala Tyr Asn Ile Ile Gly Glu Ser Pro Ala			
210	215	220	
Ser Val Pro Val Glu Val Phe Val Gly Glu Ala Ala Pro Ala Met Ala			
225	230	235	240
Pro Gln Asn Ile Gln Val Thr Pro Leu Thr Ala Ser Gln Leu Glu Val			
245	250	255	
Thr Trp Asp Pro Pro Pro Glu Ser Gln Asn Gly Asn Ile Gln Gly			
260	265	270	
Tyr Lys Val Tyr Tyr Trp Glu Ala Asp Ser Arg Asn Glu Thr Glu Lys			
275	280	285	
Met Lys Val Leu Phe Leu Pro Glu Pro Val Val Lys Ile Lys Asp Leu			
290	295	300	
Thr Ser His Thr Lys Tyr Leu Val Ser Ile Ser Ala Phe Asn Ala Ala			
305	310	315	320
Gly Asp Gly Pro Arg Ser Asp Pro Cys Gln Gly Arg Thr His Gln Ala			
325	330	335	
Ala Pro Gly Pro Pro Ser Phe Leu Glu Phe Ser Glu Ile Thr Ser Thr			
340	345	350	
Thr Leu Asn Val Ser Trp Gly Glu Pro Ser Ala Ala Asn Gly Ile Leu			
355	360	365	
Gln Gly Tyr Arg Val Val Tyr Glu Pro Leu Ala Pro Val Gln Gly Val			
370	375	380	
Ser Lys Val Val Thr Val Asp Val Lys Gly Asn Trp Gln Arg Trp Leu			
385	390	395	400
Lys Val Arg Asp Leu Thr Lys Gly Val Thr Tyr Phe Phe Arg Val Gln			
405	410	415	
Ala Arg Thr Ile Ala Tyr Gly Pro Glu Leu Gln Ala Asn Val Thr Ala			
420	425	430	
Gly Pro Ala Glu Gly Ser Pro Gly Ser Pro Arg Asn Val Leu Val Thr			
435	440	445	
Lys Ser Ala Ser Glu Leu Thr Leu Gln Trp Thr Glu Gly Asn Thr Gly			
450	455	460	

Asn Thr Pro Thr Thr Gly Tyr Val Ile Glu Ala Arg Pro Ser Asp Glu  
 465 470 475 480  
 Gly Leu Trp Asp Met Phe Ala Lys Asp Ile Pro Arg Ser Ala Thr Ser  
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 Tyr Thr Val Gly Leu Asp Lys Leu Arg Gln Gly Val Thr Tyr Glu Phe  
 500 505 510  
 Arg Val Val Ala Val Asn Lys Ala Gly Phe Gly Glu Pro Ser Arg Pro  
 515 520 525  
 Ser Ile Ala Val Ser Ala Gln Ala Glu Ala Pro Phe Tyr Glu Glu Trp  
 530 535 540  
 Trp Phe Leu Leu Val Ile Ala Leu Ser Ser Leu Leu Leu Val Leu Leu  
 545 550 555 560  
 Val Val Phe Val Leu Val His Gly Gln Ser Lys Lys Tyr Lys Asn  
 565 570 575  
 Cys Gly Ser Gly Lys Gly Ile Ser Asn Met Glu Glu Thr Val Thr Leu  
 580 585 590  
 Asp Asn Gly Gly Phe Ala Ala Leu Glu Leu Asn Ser Arg His Leu Asn  
 595 600 605  
 Val Lys Ser Thr Phe Ser Lys Lys Asn Gly Thr Arg Ser Pro Pro Arg  
 610 615 620  
 Pro Ser Pro Gly Gly Leu His Tyr Ser Asp Glu Asp Ile Cys Asn Lys  
 625 630 635 640  
 Tyr Asn Gly Ala Val Leu Thr Glu Ser Val Asn Leu Lys Glu Lys Ser  
 645 650 655  
 Val Asp Gly Ser Glu Ser Glu Ala Ser Asp Ser Asp Tyr Glu Glu Ala  
 660 665 670  
 Leu Pro Lys His Ser Phe Val Asn His Tyr Met Ser Asp Pro Thr Tyr  
 675 680 685  
 Tyr Asn Phe Trp Lys Arg Arg Pro Pro Ala Ala Ala Pro His Arg Tyr  
 690 695 700  
 Glu Ala Val Ala Gly Ala Glu Ala Gly Pro His Leu His Thr Val Ile  
 705 710 715 720  
 Thr Thr Gln Ser Ala Gly Gly Val Tyr Thr Pro Ala Gly Pro Gly Ala  
 725 730 735  
 Arg Ala Pro Leu Thr Gly Phe Ser Ser Phe Val  
 740 745

<210> 37  
 <211> 205  
 <212> PRT  
 <213> Mouse

<400> 37

Met	Leu	Gly	Thr	Leu	Val	Trp	Met	Leu	Ala	Val	Gly	Phe	Leu	Leu	Ala		
1							5							10		15	
Leu	Ala	Pro	Gly	Arg	Ala	Ala	Gly	Ala	Leu	Arg	Thr	Gly	Arg	Arg	Pro		
														20	25	30	
Ala	Arg	Pro	Arg	Asp	Cys	Ala	Asp	Arg	Pro	Glu	Glu	Leu	Leu	Gln			
														35	40	45	
Leu	Tyr	Gly	Arg	Leu	Ala	Ala	Gly	Val	Leu	Ser	Ala	Phe	His	His	Thr		
														50	55	60	
Leu	Gln	Leu	Gly	Pro	Arg	Glu	Gln	Ala	Arg	Asn	Ala	Ser	Cys	Pro	Ala		
														65	70	75	80
Gly	Gly	Arg	Ala	Ala	Asp	Arg	Arg	Phe	Arg	Pro	Pro	Thr	Asn	Leu	Arg		
														85	90	95	
Ser	Val	Ser	Pro	Trp	Ala	Tyr	Arg	Ile	Ser	Tyr	Asp	Pro	Ala	Arg	Phe		
														100	105	110	

Pro Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr  
 115 120 125  
 Gly Leu Tyr Gly Glu Glu Asp Phe Arg Phe Arg Ser Thr Pro Val Phe  
 130 135 140  
 Ser Pro Ala Val Val Leu Arg Arg Thr Ala Ala Cys Ala Gly Gly Arg  
 145 150 155 160  
 Ser Val Tyr Ala Glu His Tyr Ile Thr Ile Pro Val Gly Cys Thr Cys  
 165 170 175  
 Val Pro Glu Pro Asp Lys Ser Ala Asp Ser Ala Asn Ser Ser Met Asp  
 180 185 190  
 Lys Leu Leu Leu Gly Pro Ala Asp Arg Pro Ala Gly Arg  
 195 200 205

&lt;210&gt; 38

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 38

Met Leu Cys Phe Leu Arg Gly Met Ala Phe Val Pro Phe Leu Leu Val  
 1 5 10 15  
 Thr Trp Ser Ser Ala Ala Phe Ile Ile Ser Tyr Val Val Ala Val Leu  
 20 25 30  
 Ser Gly His Val Asn Pro Phe Leu Pro Tyr Ile Ser Asp Thr Gly Thr  
 35 40 45  
 Thr Pro Pro Glu Ser Gly Ile Phe Gly Phe Met Ile Asn Phe Ser Ala  
 50 55 60  
 Phe Leu Gly Ala Ala Thr Met Tyr Thr Arg Tyr Lys Ile Val Glu Lys  
 65 70 75 80  
 Gln Asn Glu Thr Cys Tyr Phe Ser Thr Pro Val Phe Asn Leu Val Ser  
 85 90 95  
 Leu Ala Leu Gly Leu Val Gly Cys Ile Gly Met Gly Ile Val Ala Asn  
 100 105 110  
 Phe Gln Glu Leu Ala Val Pro Val Val His Asp Gly Gly Ala Leu Leu  
 115 120 125  
 Ala Phe Val Cys Gly Val Val Tyr Thr Leu Leu Gln Ser Ile Ile Ser  
 130 135 140  
 Tyr Lys Ser Cys Pro Gln Trp Asn Ser Leu Thr Thr Cys His Val Arg  
 145 150 155 160  
 Met Ala Ile Ser Ala Val Ser Cys Ala Ala Val Val Pro Met Ile Ala  
 165 170 175  
 Cys Ala Ser Leu Ile Ser Ile Thr Lys Leu Glu Trp Asn Pro Lys Glu  
 180 185 190  
 Lys Asp Tyr Ile Tyr His Val Val Ser Ala Ile Cys Glu Trp Thr Val  
 195 200 205  
 Ala Phe Gly Phe Ile Phe Tyr Phe Leu Thr Phe Ile Gln Asp Phe Gln  
 210 215 220  
 Ser Val Thr Leu Arg Ile Ser Thr Glu Ile Asn Asp Asp Phe  
 225 230 235

&lt;210&gt; 39

&lt;211&gt; 492

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 39

Leu Arg Leu Leu Leu Ala Trp Val Ala Ala Val Pro Ala Leu Gly Gln

1	5	10	15
Val Pro Trp Thr Pro Glu Pro Arg Ala Ala Cys Gly Pro Ser Ser Cys			
20	25	30	
Tyr Ala Leu Phe Pro Arg Arg Arg Thr Phe Leu Glu Ala Trp Arg Ala			
35	40	45	
Cys Arg Glu Leu Gly Gly Asn Leu Ala Thr Pro Arg Thr Pro Glu Glu			
50	55	60	
Ala Gln Arg Val Asp Ser Leu Val Gly Val Gly Pro Ala Asn Gly Leu			
65	70	75	80
Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Pro Gln Arg			
85	90	95	
Pro Leu Arg Gly Phe Ile Trp Thr Thr Gly Asp Gln Asp Thr Ala Phe			
100	105	110	
Thr Asn Trp Ala Gln Pro Ala Thr Glu Gly Pro Cys Pro Ala Gln Arg			
115	120	125	
Cys Ala Ala Leu Glu Ala Ser Gly Glu His Arg Trp Leu Glu Gly Ser			
130	135	140	
Cys Thr Leu Ala Val Asp Gly Tyr Leu Cys Gln Phe Gly Phe Glu Gly			
145	150	155	160
Ala Cys Pro Ala Leu Pro Leu Glu Val Gly Gln Ala Gly Pro Ala Val			
165	170	175	
Tyr Thr Thr Pro Phe Asn Leu Val Ser Ser Glu Phe Glu Trp Leu Pro			
180	185	190	
Phe Gly Ser Val Ala Ala Val Gln Cys Gln Ala Gly Arg Gly Ala Ser			
195	200	205	
Leu Leu Cys Val Lys Gln Pro Ser Gly Gly Val Gly Trp Ser Gln Thr			
210	215	220	
Gly Pro Leu Cys Pro Gly Thr Gly Cys Gly Pro Asp Asn Gly Gly Cys			
225	230	235	240
Glu His Glu Cys Val Glu Glu Val Asp Gly Ala Val Ser Cys Arg Cys			
245	250	255	
Ser Glu Gly Phe Arg Leu Ala Ala Asp Gly His Ser Cys Glu Asp Pro			
260	265	270	
Cys Ala Gln Ala Pro Cys Glu Gln Gln Cys Glu Pro Gly Gly Pro Gln			
275	280	285	
Gly Tyr Ser Cys His Cys Arg Leu Gly Phe Arg Pro Ala Glu Asp Asp			
290	295	300	
Pro His Arg Cys Val Asp Thr Asp Glu Cys Gln Ile Ala Gly Val Cys			
305	310	315	320
Gln Gln Met Cys Val Asn Tyr Val Gly Gly Phe Glu Cys Tyr Cys Ser			
325	330	335	
Glu Gly His Glu Leu Glu Ala Asp Gly Ile Ser Cys Ser Pro Ala Gly			
340	345	350	
Ala Met Gly Ala Gln Ala Ser Gln Asp Leu Arg Asp Glu Leu Leu Asp			
355	360	365	
Asp Gly Glu Glu Gly Glu Asp Glu Glu Glu Pro Trp Glu Asp Phe Asp			
370	375	380	
Gly Thr Trp Thr Glu Glu Gln Gly Ile Leu Trp Leu Ala Pro Thr His			
385	390	395	400
Pro Pro Asp Phe Gly Leu Pro Tyr Arg Pro Asn Phe Pro Gln Asp Gly			
405	410	415	
Glu Pro Gln Arg Leu His Leu Glu Pro Thr Trp Pro Pro Pro Leu Lys			
420	425	430	
Ala Pro Lys Gly Pro Gln Gln Pro Pro Arg Gly Ala Ala Lys Thr Pro			
435	440	445	
Lys Gly Asn Pro Ala Asn Pro Thr His Thr Thr Phe Cys Pro Gln Asp			
450	455	460	

Leu Cys Tyr Phe Ser Tyr Thr Pro Thr Pro Glu Pro Cys Pro Pro Thr  
 465                  470                  475                  480  
 Cys His Gly Pro Cys His Thr Ser Ser Cys Val Leu  
 485                  490

<210> 40  
<211> 464  
<212> PRT  
<213> Mouse

<400> 40  
 Met Gly Arg Ala Trp Gly Leu Leu Val Gly Leu Leu Gly Val Val Trp  
 1                  5                  10                  15  
 Leu Leu Arg Leu Gly His Gly Glu Glu Arg Arg Pro Glu Thr Ala Ala  
 20                  25                  30  
 Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp Cys Thr Cys  
 35                  40                  45  
 Asp Val Glu Thr Ile Asp Lys Phe Asn Asn Tyr Arg Leu Phe Pro Arg  
 50                  55                  60  
 Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg Tyr Tyr Lys Val Asn  
 65                  70                  75                  80  
 Leu Lys Lys Pro Cys Pro Phe Trp Asn Asp Ile Asn Gln Cys Gly Arg  
 85                  90                  95  
 Arg Asp Cys Ala Val Lys Pro Cys His Ser Asp Glu Val Pro Asp Gly  
 100                105                110  
 Ile Lys Ser Ala Ser Tyr Lys Tyr Ser Glu Glu Ala Asn Arg Ile Glu  
 115                120                125  
 Glu Cys Glu Gln Ala Glu Arg Leu Gly Ala Val Asp Glu Ser Leu Ser  
 130                135                140  
 Glu Glu Thr Gln Lys Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser  
 145                150                155                160  
 Ser Asp Ser Phe Cys Glu Ile Asp Asp Ile Gln Ser Pro Asp Ala Glu  
 165                170                175  
 Tyr Val Asp Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly  
 180                185                190  
 Pro Asp Ala Trp Arg Ile Trp Ser Val Ile Tyr Glu Glu Asn Cys Phe  
 195                200                205  
 Lys Pro Gln Thr Ile Gln Arg Pro Leu Ala Ser Gly Arg Gly Lys Ser  
 210                215                220  
 Lys Glu Asn Thr Phe Tyr Asn Trp Leu Glu Gly Leu Cys Val Glu Lys  
 225                230                235                240  
 Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His Ala Ser Ile Asn Val  
 245                250                255  
 His Leu Ser Ala Arg Tyr Leu Leu Gln Asp Thr Trp Leu Glu Lys Lys  
 260                265                270  
 Trp Gly His Asn Val Thr Glu Phe Gln Gln Arg Phe Asp Gly Ile Leu  
 275                280                285  
 Thr Glu Gly Glu Gly Pro Arg Arg Leu Arg Asn Leu Tyr Phe Leu Tyr  
 290                295                300  
 Leu Ile Glu Leu Arg Ala Leu Ser Lys Val Leu Pro Phe Phe Glu Arg  
 305                310                315                320  
 Pro Asp Phe Gln Leu Phe Thr Gly Asn Lys Val Gln Asp Ala Glu Asn  
 325                330                335  
 Lys Ala Leu Leu Leu Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu  
 340                345                350  
 His Phe Asp Glu Asn Ser Phe Phe Ala Gly Asp Lys Asn Glu Ala His  
 355                360                365

Lys Leu Lys Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile  
 370                   375                   380  
 Met Asp Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln  
 385                   390                   395                   400  
 Thr Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu  
 405                   410                   415  
 Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe Gln Leu Thr  
 420                   425                   430  
 Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile Ser Thr  
 435                   440                   445  
 Ser Val Arg Glu Leu Glu Asn Phe Arg His Leu Leu Gln Asn Val His  
 450                   455                   460

<210> 41  
 <211> 148  
 <212> PRT  
 <213> Rat

<400> 41  
 Leu Asn Trp Gln Ile Lys Lys Tyr Asp Thr Lys Ala Ala Tyr Cys Gln  
 1                   5                   10                   15  
 Ser Lys Leu Ala Val Val Leu Phe Thr Lys Glu Leu Ser Arg Arg Leu  
 20                   25                   30  
 Gln Gly Thr Gly Val Thr Val Asn Ala Leu His Pro Gly Val Ala Arg  
 35                   40                   45  
 Thr Glu Leu Gly Arg His Thr Gly Met His Asn Ser Ala Phe Ser Gly  
 50                   55                   60  
 Phe Met Leu Gly Pro Phe Phe Trp Leu Leu Phe Lys Ser Pro Gln Leu  
 65                   70                   75                   80  
 Ala Ala Gln Pro Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Glu Ser  
 85                   90                   95  
 Val Ser Gly Lys Tyr Phe Asp Gly Leu Arg Glu Lys Ala Pro Ser Pro  
 100                  105                  110  
 Glu Ala Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Thr Glu Ser Ala  
 115                  120                  125  
 His Leu Val Gly Leu Asp Met Ala His Gly Ser Ser Gly Arg Gly His  
 130                  135                  140  
 Ser Ile Ser Arg  
 145

<210> 42  
 <211> 228  
 <212> PRT  
 <213> Mouse

<400> 42  
 Met Gly Phe Leu Leu Leu Leu Leu His Ala Ala Ile Ala Gly His  
 1                   5                   10                   15  
 Lys Asn Tyr Gly Thr His Asn His Cys Trp Leu Ser Leu His Arg Gly  
 20                  25                  30  
 Phe Ile Trp Ser Phe Leu Gly Pro Ala Ala Ile Ile Leu Ile Asn  
 35                  40                  45  
 Leu Val Phe Tyr Phe Leu Ile Ile Trp Ile Leu Arg Ser Lys Leu Ser  
 50                  55                  60  
 Ser Leu Asn Lys Glu Val Ser Thr Leu Gln Asp Thr Lys Val Met Thr  
 65                  70                  75                  80  
 Phe Lys Ala Ile Val Gln Leu Phe Val Leu Gly Cys Ser Trp Gly Ile

	85		90		95
Gly Leu Phe Ile Phe Ile Glu Val Gly Lys Thr Val Arg Leu Ile Val					
100		105		110	
Ala Tyr Leu Phe Thr Ile Ile Asn Val Leu Gln Gly Val Leu Ile Phe					
115		120		125	
Met Val His Cys Leu Leu Asn Arg Gln Val Arg Met Glu Tyr Lys Lys					
130		135		140	
Trp Phe His Arg Leu Arg Lys Glu Val Glu Ser Glu Ser Thr Glu Val					
145		150		155	
Ser His Ser Thr Thr His Thr Lys Met Gly Leu Ser Leu Asn Leu Glu					
165		170		175	
Asn Phe Cys Pro Thr Gly Asn Leu His Asp Pro Ser Asp Ser Ile Leu					
180		185		190	
Pro Ser Thr Glu Val Ala Gly Val Tyr Leu Ser Thr Pro Arg Ser His					
195		200		205	
Met Gly Ala Glu Asp Val Asn Ser Gly Thr His Ala Tyr Trp Ser Arg					
210		215		220	
Thr Ile Ser Asp					
225					

<210> 43  
<211> 373  
<212> PRT  
<213> Mouse

245	250	255
Tyr Arg Glu Leu Gln Arg Leu Gly Leu	Gly Asn Asn Arg Ile Thr Asp	
260	265	270
Ile Glu Asn Gly Thr Phe Ala Asn Ile Pro Arg Val Arg Glu Ile His		
275	280	285
Leu Glu His Asn Lys Leu Lys Lys Ile Pro Ser Gly Leu Gln Glu Leu		
290	295	300
Lys Tyr Leu Gln Ile Ile Phe Leu His Tyr Asn Ser Ile Ala Lys Val		
305	310	315
Gly Val Asn Asp Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu		320
325	330	335
Tyr Ser Ala Ile Ser Leu Phe Asn Asn Pro Met Lys Tyr Trp Glu Ile		
340	345	350
Gln Pro Ala Thr Phe Arg Cys Val Leu Gly Arg Met Ser Val Gln Leu		
355	360	365
Gly Asn Val Gly Lys		
370		

<210> 44  
<211> 466  
<212> PRT  
<213> Mouse

<400> 44		
Met Trp Gly Cys Trp Leu Gly Leu Leu Leu Leu Ala Gly Gln		
1	5	10
Ala Ala Leu Glu Ala Arg Arg Ser Arg Trp Arg Arg Glu Leu Ala Pro		
20	25	30
Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys Gln		
35	40	45
Glu Gln Asp Met Cys Cys Arg Gly Arg Ala Asp Glu Cys Ala Leu Pro		
50	55	60
Tyr Leu Gly Ala Thr Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr Val		
65	70	75
Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Ile Pro Pro		
85	90	95
Pro Phe Pro Pro Val Gln Gly Cys Met His Gly Gly Arg Ile Tyr Pro		
100	105	110
Val Phe Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys His Glu		
115	120	125
Gly Gly His Trp Glu Cys Asp Gln Glu Pro Cys Leu Val Asp Pro Asp		
130	135	140
Met Ile Lys Ala Ile Asn Arg Gly Asn Tyr Gly Trp Gln Ala Gly Asn		
145	150	155
His Ser Ala Phe Trp Gly Met Thr Leu Asp Glu Gly Ile Arg Tyr Arg		
165	170	175
Leu Gly Thr Ile Arg Pro Ser Ser Thr Val Met Asn Met Asn Glu Ile		
180	185	190
Tyr Thr Val Leu Gly Gln Gly Glu Val Leu Pro Thr Ala Phe Glu Ala		
195	200	205
Ser Glu Lys Trp Pro Asn Leu Ile His Glu Pro Leu Asp Gln Gly Asn		
210	215	220
Cys Ala Gly Ser Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp Arg		
225	230	235
Val Ser Ile His Ser Leu Gly His Met Thr Pro Ile Leu Ser Pro Gln		240
245	250	255
Asn Leu Leu Ser Cys Asp Thr His His Gln Gln Gly Cys Arg Gly Gly		

260	265	270
Arg Leu Asp Gly Ala Trp Trp Phe Leu Arg Arg Arg Gly Val Val Ser		
275	280	285
Asp Asn Cys Tyr Pro Phe Ser Gly Arg Glu Gln Asn Glu Ala Ser Pro		
290	295	300
Thr Pro Arg Cys Met Met His Ser Arg Ala Met Gly Arg Gly Lys Arg		
305	310	315
Gln Ala Thr Ser Arg Cys Pro Asn Gly Gln Val Asp Ser Asn Asp Ile		
325	330	335
Tyr Gln Val Thr Pro Ala Tyr Arg Leu Gly Ser Asp Glu Lys Glu Ile		
340	345	350
Met Lys Glu Leu Met Glu Asn Gly Pro Val Gln Ala Leu Met Glu Val		
355	360	365
His Glu Asp Phe Phe Leu Tyr Gln Arg Gly Ile Tyr Ser His Thr Pro		
370	375	380
Val Ser Gln Gly Arg Pro Glu Gln Tyr Arg Arg His Gly Thr His Ser		
385	390	395
Val Lys Ile Thr Gly Trp Gly Glu Glu Thr Leu Pro Asp Gly Arg Thr		
405	410	415
Ile Lys Tyr Trp Thr Ala Ala Asn Ser Trp Gly Pro Trp Trp Gly Glu		
420	425	430
Arg Gly His Phe Arg Ile Val Arg Gly Thr Asn Glu Cys Asp Ile Glu		
435	440	445
Thr Phe Val Leu Gly Val Trp Gly Arg Val Gly Met Glu Asp Met Gly		
450	455	460
His His		
465		

<210> 45  
<211> 422  
<212> PRT  
<213> Mouse

<400> 45		
Met Asp Phe Trp Leu Trp Leu Leu Tyr Phe Leu Pro Val Ser Gly Ala		
1	5	10
Leu Arg Val Leu Pro Glu Val Gln Leu Asn Val Glu Trp Gly Gly Ser		
20	25	30
Ile Ile Ile Glu Cys Pro Leu Pro Gln Leu His Val Arg Met Tyr Leu		
35	40	45
Cys Arg Gln Met Ala Lys Pro Gly Ile Cys Ser Thr Val Val Ser Asn		
50	55	60
Thr Phe Val Lys Lys Glu Tyr Glu Arg Arg Val Thr Leu Thr Pro Cys		
65	70	75
Leu Asp Lys Lys Leu Phe Leu Val Glu Met Thr Gln Leu Thr Glu Asn		
85	90	95
Asp Asp Gly Ile Tyr Ala Cys Gly Val Gly Met Lys Thr Asp Lys Gly		
100	105	110
Lys Thr Gln Lys Ile Thr Leu Asn Val His Asn Glu Tyr Pro Glu Pro		
115	120	125
Phe Trp Glu Asp Glu Trp Thr Ser Glu Arg Pro Arg Trp Leu His Arg		
130	135	140
Phe Leu Gln His Gln Met Pro Trp Leu His Gly Ser Glu His Pro Ser		
145	150	155
Ser Ser Gly Val Ile Ala Lys Val Thr Thr Pro Ala Ser Lys Thr Glu		
165	170	175
Ala Pro Pro Val His Gln Pro Ser Ser Ile Thr Ser Val Thr Gln His		

	180	185	190
Pro Arg Val Tyr Arg Ala Phe Ser Val Ser Ala Thr Lys Ser Pro Ala			
195	200	205	
Leu Leu Pro Ala Thr Thr Ala Ser Lys Thr Ser Thr Gln Gln Ala Ile			
210	215	220	
Arg Pro Leu Glu Ala Ser Tyr Ser His His Thr Arg Leu His Glu Gln			
225	230	235	240
Arg Thr Arg His His Gly Pro His Tyr Gly Arg Glu Asp Arg Gly Leu			
245	250	255	
His Ile Pro Ile Pro Glu Phe His Ile Leu Ile Pro Thr Phe Leu Gly			
260	265	270	
Phe Leu Leu Leu Val Leu Leu Gly Leu Val Val Lys Arg Ala Ile Gln			
275	280	285	
Arg Arg Arg Ala Ser Ser Arg Arg Ala Gly Arg Leu Ala Met Arg Arg			
290	295	300	
Arg Gly Arg Gly Ala Ser Arg Pro Phe Pro Thr Gln Arg Arg Asp Ala			
305	310	315	320
Pro Gln Arg Pro Arg Ser Gln Asn Asn Val Tyr Ser Ala Cys Pro Arg			
325	330	335	
Arg Ala Arg Gly Pro Asp Ser Leu Gly Pro Ala Glu Ala Pro Leu Leu			
340	345	350	
Asn Ala Pro Ala Ser Ala Ser Pro Ala Ser Pro Gln Val Leu Glu Ala			
355	360	365	
Pro Trp Pro His Thr Pro Ser Leu Lys Met Ser Cys Glu Tyr Val Ser			
370	375	380	
Leu Gly Tyr Gln Pro Ala Val Asn Leu Glu Asp Pro Asp Ser Asp Asp			
385	390	395	400
Tyr Ile Asn Ile Pro Asp Pro Ser His Leu Pro Ser Tyr Ala Pro Gly			
405	410	415	
Pro Arg Ser Ser Cys Gln			
420			

<210> 46  
<211> 228  
<212> PRT  
<213> Mouse

<400> 46			
Met Lys Ala Leu Arg Ala Val Leu Leu Ile Leu Leu Ser Gly Gln			
1	5	10	15
Pro Gly Ser Gly Trp Ala Gln Glu Asp Gly Asp Ala Asp Pro Glu Pro			
20	25	30	
Glu Asn Tyr Asn Tyr Asp Asp Asp Asp Asp Glu Glu Glu Glu Glu			
35	40	45	
Thr Asn Met Ile Pro Gly Ser Arg Asp Arg Ala Pro Leu Gln Cys Tyr			
50	55	60	
Phe Cys Gln Val Leu His Ser Gly Glu Ser Cys Asn Gln Thr Gln Ser			
65	70	75	80
Cys Ser Ser Ser Lys Pro Phe Cys Ile Thr Leu Val Ser His Ser Gly			
85	90	95	
Thr Asp Lys Gly Tyr Leu Thr Thr Tyr Ser Met Trp Cys Thr Asp Thr			
100	105	110	
Cys Gln Pro Ile Ile Lys Thr Val Gly Gly Thr Gln Met Thr Gln Thr			
115	120	125	
Cys Cys Gln Ser Thr Leu Cys Asn Ile Pro Pro Trp Gln Asn Pro Gln			
130	135	140	
Val Gln Asn Pro Leu Gly Gly Arg Ala Asp Ser Pro Leu Glu Ser Gly			

145	150	155	160
Thr Arg His Pro Gln Gly Gly Lys Phe Ser His Pro Gln Val Val Lys			
165	170	175	
Ala Ala His Pro Gln Ser Asp Gly Ala Asn Leu Pro Lys Ser Gly Lys			
180	185	190	
Ala Asn Gln Pro Gln Gly Ser Gly Ala Gly Tyr Pro Ser Gly Trp Thr			
195	200	205	
Lys Phe Gly Asn Ile Ala Leu Leu Ser Phe Phe Thr Cys Leu Trp			
210	215	220	
Ala Ser Gly Ala			
225			

<210> 47  
<211> 269  
<212> PRT  
<213> Mouse

<400> 47			
Gly Cys Ser Asp Gly Glu Asn Gln Arg Ser Gly His Leu Ser Val Ser			
1	5	10	15
Leu Gln Leu Ser Leu Lys Val Leu Leu Ile Arg Met Ala Ser Gly Trp			
20	25	30	
Phe Tyr Leu Ser Cys Met Val Leu Gly Ser Leu Gly Ser Met Cys Ile			
35	40	45	
Leu Phe Thr Ala Tyr Trp Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp			
50	55	60	
Asp Gly Thr Val Leu Met Phe Asn Trp His Pro Val Leu Met Val Ala			
65	70	75	80
Gly Met Val Val Leu Tyr Gly Ala Ala Ser Leu Val Tyr Arg Leu Pro			
85	90	95	
Ser Ser Trp Val Gly Pro Arg Leu Pro Trp Lys Val Leu His Ala Ala			
100	105	110	
Leu His Leu Leu Ala Phe Thr Cys Thr Val Val Gly Leu Ile Ala Val			
115	120	125	
Phe Arg Phe His Asn His Ser Arg Ile Ala His Leu Tyr Ser Leu His			
130	135	140	
Ser Trp Leu Gly Ile Thr Thr Val Val Leu Phe Ala Cys Gln Trp Phe			
145	150	155	160
Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala Ser Gln Trp Leu Arg			
165	170	175	
Ser Leu Leu Lys Pro Leu His Val Phe Phe Gly Ala Cys Ile Leu Ser			
180	185	190	
Leu Ser Ile Thr Ser Val Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe			
195	200	205	
Val Leu Lys Asn Ala Thr Lys Pro Tyr Ser Ser Leu Pro Gly Glu Ala			
210	215	220	
Val Phe Ala Asn Ser Thr Gly Leu Leu Val Val Ala Phe Gly Leu Leu			
225	230	235	240
Val Leu Tyr Val Leu Leu Ala Ser Ser Trp Lys Arg Pro Asp Pro Gly			
245	250	255	
Ala Leu Thr Asp Arg Gln Pro Leu Leu His Asp Arg Glu			
260	265		

<210> 48  
<211> 188  
<212> PRT  
<213> Mouse

&lt;400&gt; 48

Met	Arg	Leu	Pro	Leu	Pro	Leu	Leu	Leu	Phe	Gly	Cys	Arg	Ala	Ile	
1		5				10						15			
Leu	Gly	Ser	Ala	Gly	Asp	Arg	Val	Ser	Leu	Ser	Ala	Ser	Ala	Pro	Thr
						20		25						30	
Leu	Asp	Asp	Glu	Glu	Lys	Tyr	Ser	Ala	His	Met	Pro	Ala	His	Leu	Arg
						35		40					45		
Cys	Asp	Ala	Cys	Arg	Ala	Val	Ala	Phe	Gln	Met	Gly	Gln	Arg	Leu	Ala
						50		55			60				
Lys	Ala	Glu	Ala	Lys	Ser	His	Thr	Pro	Asp	Ala	Ser	Gly	Leu	Gln	Glu
						65		70		75			80		
Leu	Ser	Glu	Ser	Thr	Tyr	Thr	Asp	Val	Leu	Asp	Gln	Thr	Cys	Ser	Gln
						85			90			95			
Asn	Trp	Gln	Ser	Tyr	Gly	Val	His	Glu	Val	Asn	Gln	Met	Lys	Arg	Leu
						100		105				110			
Thr	Gly	Pro	Gly	Leu	Ser	Lys	Gly	Pro	Glu	Pro	Arg	Ile	Ser	Val	Met
						115		120			125				
Ile	Ser	Gly	Gly	Pro	Trp	Pro	Asn	Arg	Leu	Ser	Lys	Thr	Cys	Phe	His
						130		135			140				
Tyr	Leu	Gly	Glu	Phe	Gly	Glu	Asp	Gln	Ile	Tyr	Glu	Ala	Tyr	Arg	Gln
						145		150		155			160		
Gly	Gln	Ala	Asn	Leu	Glu	Ala	Leu	Leu	Cys	Gly	Gly	Thr	His	Gly	Pro
						165			170			175			
Cys	Ser	Gln	Glu	Ile	Leu	Ala	Gln	Arg	Glu	Glu	Leu				
						180			185						

&lt;210&gt; 49

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 49

Met	Ile	Pro	Gln	Val	Val	Thr	Ser	Glu	Thr	Val	Thr	Val	Ile	Ser	Pro
1				5				10				15			
Asn	Gly	Ile	Ser	Phe	Pro	Gln	Thr	Asp	Lys	Pro	Gln	Pro	Ser	His	Gln
						20		25				30			
Ser	Gln	Asp	Arg	Leu	Lys	Lys	His	Leu	Lys	Ala	Glu	Ile	Lys	Val	Met
						35		40			45				
Ala	Ala	Ile	Gln	Ile	Met	Cys	Ala	Val	Met	Val	Leu	Ser	Leu	Gly	Ile
						50		55			60				
Ile	Leu	Ala	Ser	Val	Pro	Ser	Asn	Leu	His	Phe	Thr	Ser	Val	Phe	Ser
						65		70		75			80		
Ile	Leu	Leu	Glu	Ser	Gly	Tyr	Pro	Phe	Val	Gly	Ala	Leu	Phe	Phe	Ala
						85		90			95				
Ile	Ser	Gly	Ile	Leu	Ser	Ile	Val	Thr	Glu	Lys	Lys	Met	Thr	Lys	Pro
						100		105			110				
Leu	Val	His	Ser	Ser	Leu	Ala	Leu	Ser	Ile	Leu	Ser	Val	Leu	Ser	Ala
						115		120			125				
Leu	Thr	Gly	Ile	Ala	Ile	Leu	Ser	Val	Ser	Leu	Ala	Leu	Glu	Pro	
						130		135			140				
Ala	Leu	Gln	Gln	Cys	Lys	Leu	Ala	Phe	Thr	Gln	Leu	Asp	Thr	Thr	Gln
						145		150		155			160		
Asp	Ala	Tyr	His	Phe	Phe	Ser	Pro	Glu	Pro	Leu	Asn	Ser	Cys	Phe	Val
						165			170			175			
Ala	Lys	Ala	Ala	Leu	Thr	Gly	Val	Phe	Ser	Leu	Met	Leu	Ile	Ser	Ser
						180			185			190			

Val Leu Glu Leu Gly Leu Ala Val Leu Thr Ala Thr Leu Trp Trp Lys  
 195 200 205  
 Gln Ser Ser Ser Ala Phe Ser Gly Asn Val Ile Phe Leu Ser Gln Asn  
 210 215 220  
 Ser Lys Asn Lys Ser Ser Val Ser Ser Glu Ser Leu Cys Asn Pro Thr  
 225 230 235 240  
 Tyr Glu Asn Ile Leu Thr Ser  
 245

<210> 50  
 <211> 182  
 <212> PRT  
 <213> Mouse

<400> 50  
 Pro Phe His Cys His Val Trp Ser Leu Cys Leu Gln Gly Ser Lys Gln  
 1 5 10 15  
 Ser Gly Leu Cys Gln Val Gln Arg Asp Leu Gly Arg Asp Asp Arg Ser  
 20 25 30  
 Val Arg Gly Ser Lys Ala Ala Val Val Ala Gly Ala Val Val Gly Thr  
 35 40 45  
 Phe Val Gly Leu Val Leu Ile Ala Gly Leu Val Leu Leu Tyr Gln Arg  
 50 55 60  
 Arg Ser Lys Thr Leu Glu Glu Leu Ala Asn Asp Ile Lys Glu Asp Ala  
 65 70 75 80  
 Ile Ala Pro Arg Thr Leu Pro Trp Thr Lys Gly Ser Asp Thr Ile Ser  
 85 90 95  
 Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg Pro  
 100 105 110  
 Pro Lys Ala Ala Pro Pro Arg Pro Gly Thr Phe Thr Pro Thr Pro Ser  
 115 120 125  
 Val Ser Ser Gln Ala Leu Ser Ser Pro Arg Leu Pro Arg Val Asp Glu  
 130 135 140  
 Pro Pro Pro Gln Ala Val Ser Leu Thr Pro Gly Gly Val Ser Ser Ser  
 145 150 155 160  
 Ala Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 165 170 175  
 Gln Ala Gly Ser Leu Val  
 180

<210> 51  
 <211> 248  
 <212> PRT  
 <213> Mouse

<400> 51  
 Met Ser Trp Ser Pro Ile Leu Pro Phe Leu Ser Leu Leu Leu Leu  
 1 5 10 15  
 Phe Pro Leu Glu Val Pro Arg Ala Ala Thr Ala Ser Leu Ser Gln Ala  
 20 25 30  
 Ser Ser Glu Gly Thr Thr Cys Lys Val His Asp Val Cys Leu Leu  
 35 40 45  
 Gly Pro Arg Pro Leu Pro Pro Ser Pro Pro Val Arg Val Ser Leu Tyr  
 50 55 60  
 Tyr Glu Ser Leu Cys Gly Ala Cys Arg Tyr Phe Leu Val Arg Asp Leu  
 65 70 75 80  
 Phe Pro Thr Trp Leu Met Val Met Glu Ile Met Asn Ile Thr Leu Val

85	90	95
Pro Tyr Gly Asn Ala Gln Glu Arg Asn Val Ser Gly Thr Trp	Glu Phe	
100	105	110
Thr Cys Gln His Gly Glu Leu Glu Cys Arg Leu Asn Met Val	Glu Ala	
115	120	125
Cys Leu Leu Asp Lys Leu Glu Lys Glu Ala Ala	Phe Leu Thr Ile Val	
130	135	140
Cys Met Glu Glu Met Asp Asp Met Glu Lys Lys Leu Gly Pro	Cys Leu	
145	150	155
Gln Val Tyr Ala Pro Glu Val Ser Pro Glu Ser Ile Met Glu	Cys Ala	
165	170	175
Thr Gly Lys Arg Gly Thr Gln Leu Met His Glu Asn Ala	Gln Leu Thr	
180	185	190
Asp Ala Leu His Pro Pro His Glu Tyr Val Pro Trp Val Leu Val	Asn	
195	200	205
Glu Lys Pro Leu Lys Asp Pro Ser Glu Leu Leu Ser Ile Val	Cys Gln	
210	215	220
Leu Asp Gln Gly Thr Glu Lys Pro Asp Ile Cys Ser Ser Ile Ala	Asp	
225	230	235
Ser Pro Arg Lys Val Cys Tyr Lys		240
	245	

<210> 52  
<211> 278  
<212> PRT  
<213> Mouse

<400> 52		
Met Gln Thr Met Trp Gly Ser Gly Glu Leu Leu Val Ala Trp Phe Leu		
1	5	10
Val Leu Ala Ala Asp Gly Thr Thr Glu His Val Tyr Arg Pro Ser Arg		
20	25	30
Arg Val Cys Thr Val Gly Ile Ser Gly Ser Ile Ser Glu Thr Phe		
35	40	45
Val Gln Arg Val Tyr Gln Pro Tyr Leu Thr Thr Cys Asp Gly His Arg		
50	55	60
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser		
65	70	75
Pro Gly Val Thr Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp		
85	90	95
Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln		
100	105	110
Pro Pro Cys Gly Asn Gly Gly Ser Cys Ile Arg Pro Gly His Cys Arg		
115	120	125
Cys Pro Val Gly Trp Gln Gly Asp Thr Cys Gln Thr Asp Val Asp Glu		
130	135	140
Cys Ser Thr Gly Glu Ala Ser Cys Pro Gln Arg Cys Val Asn Thr Val		
145	150	155
Gly Ser Tyr Trp Cys Gln Gly Trp Glu Gly Gln Ser Pro Ser Ala Asp		
165	170	175
Gly Thr Arg Cys Leu Ser Lys Glu Gly Pro Ser Pro Val Ala Pro Asn		
180	185	190
Pro Thr Ala Gly Val Asp Ser Met Ala Arg Glu Glu Val Tyr Arg Leu		
195	200	205
Gln Ala Arg Val Asp Val Leu Glu Gln Lys Leu Gln Leu Val Leu Ala		
210	215	220
Pro Leu His Ser Leu Ala Ser Arg Ser Thr Glu His Gly Leu Gln Asp		

225	230	235	240												
Pro	Gly	Ser	Leu	Leu	Ala	His	Ser	Phe	Gln	Gln	Leu	Asp	Arg	Ile	Asp
245									250					255	
Ser	Leu	Ser	Glu	Gln	Val	Ser	Phe	Leu	Glu	Glu	His	Leu	Gly	Ser	Cys
260									265					270	
Ser	Cys	Lys	Lys	Asp	Leu										
275															

<210> 53  
<211> 409  
<212> PRT  
<213> Mouse

<400> 53																
Met	Lys	Leu	Lys	Gln	Arg	Val	Val	Leu	Leu	Ala	Ile	Leu	Leu	Val	Ile	
1								10						15		
Phe	Ile	Phe	Thr	Lys	Val	Phe	Leu	Ile	Asp	Asn	Leu	Asp	Thr	Ser	Ala	
20								25						30		
Ala	Asn	Arg	Glu	Asp	Gln	Arg	Ala	Phe	His	Arg	Met	Met	Thr	Gly	Leu	
35								40						45		
Arg	Val	Glu	Leu	Val	Pro	Lys	Leu	Asp	His	Thr	Leu	Gln	Ser	Pro	Trp	
50								55						60		
Glu	Ile	Ala	Ala	Gln	Trp	Val	Val	Pro	Arg	Glu	Val	Tyr	Pro	Glu	Glu	
65								70						80		
Thr	Pro	Glu	Leu	Gly	Ala	Ile	Met	His	Ala	Met	Ala	Thr	Lys	Lys	Ile	
85								90						95		
Ile	Lys	Ala	Asp	Val	Gly	Tyr	Lys	Gly	Thr	Gln	Leu	Lys	Ala	Leu	Leu	
100								105						110		
Ile	Leu	Glu	Gly	Gly	Gln	Lys	Val	Val	Phe	Lys	Pro	Lys	Arg	Tyr	Ser	
115								120						125		
Arg	Asp	Tyr	Val	Val	Glu	Gly	Glu	Pro	Tyr	Ala	Gly	Tyr	Asp	Arg	His	
130								135						140		
Asn	Ala	Glu	Val	Ala	Ala	Phe	His	Leu	Asp	Arg	Ile	Leu	Gly	Phe	Arg	
145								150						160		
Arg	Ala	Pro	Leu	Val	Val	Gly	Arg	Tyr	Val	Asn	Leu	Arg	Thr	Glu	Val	
165								170						175		
Lys	Pro	Val	Ala	Thr	Glu	Gln	Leu	Leu	Ser	Thr	Phe	Leu	Thr	Val	Gly	
180								185						190		
Asn	Asn	Thr	Cys	Phe	Tyr	Gly	Lys	Cys	Tyr	Tyr	Cys	Arg	Glu	Thr	Glu	
195								200						205		
Pro	Ala	Cys	Ala	Asp	Gly	Asp	Met	Met	Glu	Gly	Ser	Val	Thr	Leu	Trp	
210								215						220		
Leu	Pro	Asp	Val	Trp	Pro	Leu	Gln	Lys	His	Arg	His	Pro	Trp	Gly	Arg	
225								230						235		240
Thr	Tyr	Arg	Glu	Gly	Lys	Leu	Ala	Arg	Trp	Glu	Tyr	Asp	Glu	Ser	Tyr	
245								250						255		
Cys	Asp	Ala	Val	Lys	Lys	Thr	Ser	Pro	Tyr	Asp	Ser	Gly	Pro	Arg	Leu	
260								265						270		
Leu	Asp	Ile	Ile	Asp	Thr	Ala	Val	Phe	Asp	Tyr	Leu	Ile	Gly	Asn	Ala	
275								280						285		
Asp	Arg	His	His	Tyr	Glu	Ser	Phe	Gln	Asp	Asp	Glu	Gly	Ala	Ser	Met	
290								295						300		
Leu	Ile	Leu	Leu	Asp	Asn	Ala	Lys	Ser	Phe	Gly	Asn	Pro	Ser	Leu	Asp	
305								310						315		320
Glu	Arg	Ser	Ile	Leu	Ala	Pro	Leu	Tyr	Gln	Cys	Cys	Ile	Ile	Arg	Val	
325								330						335		
Ser	Thr	Trp	Asn	Arg	Leu	Asn	Tyr	Leu	Lys	Asn	Gly	Val	Leu	Lys	Ser	

340	345	350
Ala Leu Lys Ser Ala Met Ala His Asp Pro Ile Ser Pro Val Leu Ser		
355	360	365
Asp Pro His Leu Asp Thr Val Asp Gln Arg Leu Leu Asn Val Leu Ala		
370	375	380
Thr Ile Lys Gln Cys Thr Asp Gln Phe Gly Thr Asp Thr Val Leu Val		
385	390	395
Glu Asp Arg Met Pro Leu Ser His Leu		
405		

<210> 54  
<211> 697  
<212> PRT  
<213> Mouse

<400> 54		
Met Arg Leu Thr Val Gly Ala Leu Leu Ala Cys Ala Ala Leu Gly Leu		
1	5	10
Cys Leu Ala Val Pro Asp Lys Thr Val Lys Trp Cys Ala Val Ser Glu		
20	25	30
His Glu Asn Thr Lys Cys Ile Ser Phe Arg Asp His Met Lys Thr Val		
35	40	45
Leu Pro Pro Asp Gly Pro Arg Leu Ala Cys Val Lys Lys Thr Ser Tyr		
50	55	60
Pro Asp Cys Ile Lys Ala Ile Ser Ala Ser Glu Ala Asp Ala Met Thr		
65	70	75
Leu Asp Gly Gly Trp Val Tyr Asp Ala Gly Leu Thr Pro Asn Asn Leu		
85	90	95
Lys Pro Val Ala Ala Glu Phe Tyr Gly Ser Val Glu His Pro Gln Thr		
100	105	110
Tyr Tyr Tyr Ala Val Ala Val Val Lys Lys Gly Thr Asp Phe Gln Leu		
115	120	125
Asn Gln Leu Glu Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser		
130	135	140
Ala Gly Trp Val Ile Pro Ile Gly Leu Leu Phe Cys Lys Leu Ser Glu		
145	150	155
Pro Arg Ser Pro Leu Glu Lys Ala Val Ser Ser Phe Phe Ser Gly Ser		
165	170	175
Cys Val Pro Cys Ala Asp Pro Val Ala Phe Pro Lys Leu Cys Gln Leu		
180	185	190
Cys Pro Gly Cys Gly Cys Ser Ser Thr Gln Pro Phe Phe Gly Tyr Val		
195	200	205
Gly Ala Phe Lys Cys Leu Lys Asp Gly Gly Asp Val Ala Phe Val		
210	215	220
Lys His Thr Thr Ile Phe Glu Val Leu Pro Glu Lys Ala Asp Arg Asp		
225	230	235
Gln Tyr Glu Leu Leu Cys Leu Asp Asn Thr Arg Lys Pro Val Asp Gln		
245	250	255
Tyr Glu Asp Cys Tyr Leu Ala Arg Ile Pro Ser His Ala Val Val Ala		
260	265	270
Arg Lys Asn Asn Gly Lys Glu Asp Leu Ile Trp Glu Ile Leu Lys Val		
275	280	285
Ala Gln Glu His Phe Gly Lys Lys Ser Lys Asp Phe Gln Leu Phe		
290	295	300
Ser Ser Pro Leu Gly Lys Asp Leu Leu Phe Lys Asp Ser Ala Phe Gly		
305	310	315
Leu Leu Arg Val Pro Pro Arg Met Asp Tyr Arg Leu Tyr Leu Gly His		

325	330	335
Asn Tyr Val Thr Ala Ile Arg Asn Gln Gln Glu Gly Val Cys Pro Glu		
340	345	350
Gly Ser Ile Asp Asn Ser Pro Val Lys Trp Cys Ala Leu Ser His Leu		
355	360	365
Glu Arg Thr Lys Cys Asp Glu Trp Ser Ile Ile Ser Glu Gly Lys Ile		
370	375	380
Glu Cys Glu Ser Ala Glu Thr Thr Glu Asp Cys Ile Glu Lys Ile Val		
385	390	395
Asn Gly Glu Ala Asp Ala Met Thr Leu Asp Gly Gly His Ala Tyr Ile		
405	410	415
Ala Gly Gln Cys Gly Leu Val Pro Val Met Ala Glu Tyr Tyr Glu Ser		
420	425	430
Ser Asn Cys Ala Ile Pro Ser Gln Gln Gly Ile Phe Pro Lys Gly Tyr		
435	440	445
Tyr Ala Val Ala Val Val Lys Ala Ser Asp Thr Ser Ile Thr Trp Asn		
450	455	460
Asn Leu Lys Gly Lys Lys Ser Cys His Thr Gly Val Asp Arg Thr Ala		
465	470	475
Gly Trp Asn Ile Pro Met Gly Met Leu Tyr Asn Arg Ile Asn His Cys		
485	490	495
Lys Phe Asp Glu Phe Ser Gln Gly Cys Ala Pro Gly Tyr Glu Lys		
500	505	510
Asn Ser Thr Leu Cys Asp Leu Cys Ile Gly Pro Leu Lys Cys Ala Pro		
515	520	525
Asn Asn Lys Glu Glu Tyr Asn Gly Tyr Thr Gly Ala Phe Arg Cys Leu		
530	535	540
Val Glu Lys Gly Asp Val Ala Phe Val Lys His Gln Thr Val Leu Asp		
545	550	555
Asn Thr Glu Gly Lys Asn Pro Ala Glu Trp Ala Lys Asn Leu Lys Gln		
565	570	575
Glu Asp Phe Glu Leu Leu Cys Pro Asp Gly Thr Arg Lys Pro Val Lys		
580	585	590
Asp Phe Ala Ser Cys His Leu Ala Gln Ala Pro Asn His Val Val Val		
595	600	605
Ser Arg Lys Glu Lys Ala Ala Arg Val Lys Ala Val Leu Thr Ser Gln		
610	615	620
Glu Thr Leu Phe Gly Gly Ser Asp Cys Thr Gly Asn Phe Cys Leu Phe		
625	630	635
Lys Ser Thr Thr Lys Asp Leu Leu Phe Arg Asp Asp Thr Lys Cys Phe		
645	650	655
Val Lys Leu Pro Glu Gly Thr Thr Pro Glu Lys Tyr Leu Gly Ala Glu		
660	665	670
Tyr Met Gln Ser Val Gly Asn Met Arg Lys Cys Ser Thr Ser Arg Leu		
675	680	685
Leu Glu Ala Cys Thr Phe His Lys His		
690	695	

<210> 55  
<211> 400  
<212> PRT  
<213> Mouse

<400> 55  
Gly Ala Pro Thr Pro Ala Tyr Val Arg Ser Ala Arg Arg Thr Glu Pro  
1 5 10 15  
Leu Ala Ser Gly Ala Arg Ser Arg Leu Cys Gln Cys Arg Arg Val Pro

20	25	30
Ala Arg Lys Gln Gly Pro Gln Glu Gln Gly Ser Gly Glu Ser Thr		
35	40	45
Thr Ser Ser Pro Gln Trp Trp Arg Arg Trp Arg Arg Leu Trp Ser Thr		
50	55	60
Cys Ser Cys Ser Ala Asp Asp Arg His Thr Gly Ser His Thr Asp Leu		
65	70	75
Lys Glu Glu Thr Pro Ser Trp Thr Gln Ile Ser Val Val Phe Arg Lys		
85	90	95
Asp Gly Gln Asp Glu Leu Gln Ala Ala His Lys Ala His Gly Ser Gly		
100	105	110
Ser Pro Leu Thr Asn Gln Glu Ile Pro Ser Ser Gly Ser Gly Phe		
115	120	125
Ile Val Ser Glu Asp Gly Leu Ile Val Thr Asn Ala His Val Leu Thr		
130	135	140
Asn Gln Gln Lys Ile Gln Val Glu Leu Gln Ser Gly Ala Arg Tyr Glu		
145	150	155
Ala Thr Val Lys Asp Ile Asp His Lys Leu Asp Leu Ala Leu Ile Lys		
165	170	175
Ile Glu Pro Asp Thr Glu Leu Pro Val Leu Leu Leu Gly Arg Ser Ser		
180	185	190
Asp Leu Arg Ala Gly Glu Phe Val Val Ala Leu Gly Ser Pro Phe Ser		
195	200	205
Leu Gln Asn Thr Val Thr Ala Gly Ile Val Ser Thr Thr Gln Arg Gly		
210	215	220
Gly Arg Glu Leu Gly Leu Lys Asn Ser Asp Ile Asp Tyr Ile Gln Thr		
225	230	235
Asp Ala Ile Ile Asn His Gly Asn Ser Gly Gly Pro Leu Val Asn Leu		
245	250	255
Asp Gly Asp Val Ile Gly Ile Asn Thr Leu Lys Val Thr Ala Gly Ile		
260	265	270
Ser Phe Ala Ile Pro Ser Asp Arg Ile Arg Gln Phe Leu Glu Asp Tyr		
275	280	285
His Glu Arg Gln Leu Lys Gly Lys Ala Pro Leu Gln Lys Lys Tyr Leu		
290	295	300
Gly Leu Arg Met Leu Pro Leu Thr Leu Asn Leu Leu Gln Glu Met Lys		
305	310	315
Arg Gln Asp Pro Glu Phe Pro Asp Val Ser Ser Gly Val Phe Val Tyr		
325	330	335
Glu Val Ile Gln Gly Ser Ala Ala Ser Ser Gly Leu Arg Asp His		
340	345	350
Asp Val Ile Val Ser Ile Asn Gly Gln Pro Val Thr Thr Thr Thr Asp		
355	360	365
Val Ile Glu Ala Val Lys Asp Asn Asp Phe Leu Ser Ile Ile Val Leu		
370	375	380
Arg Gly Ser Gln Thr Leu Phe Leu Thr Val Thr Pro Glu Ile Ile Asn		
385	390	400

<210> 56  
<211> 174  
<212> PRT  
<213> Mouse

<400> 56  
Met Pro Ala Cys Arg Leu Cys Leu Leu Ala Ala Gly Leu Leu Leu Gly  
1 5 10 15  
Leu Leu Leu Phe Thr Pro Ile Ser Ala Thr Gly Thr Asp Ala Glu Lys

20	25	30
Pro	Gly	Glu
Cys	Pro	Gln
Leu	Glu	Pro
Asp	Ile	Thr
Lys	Asn	Asp
Cys	Arg	Cys
Val	Cys	Leu
Ala	Gly	Glu
50	55	60
Gly	Ser	Ser
Val	Cys	Ser
Lys	Pro	Gly
Asn	Gly	Pro
Gly	Asp	Ser
85	90	95
Ser	Ala	Gly
Leu	Asp	His
Thr	Thr	Lys
Asp	Pro	Pro
Gly	Gly	Gly
100	105	110
Thr	Lys	Pro
Pro	Pro	Ala
Ala	Val	Thr
Arg	Glu	Gly
115	120	125
Gln	Gly	Thr
Thr	Cys	Pro
Cys	Pro	Ser
Val	Asp	Ile
Asp	Ile	Pro
Gly	Gly	Lys
130	135	140
Asp	Gln	Cys
Gln	Cys	Gln
Val	Asp	Ser
145	150	155
Arg	Asn	Gly
Gly	Cys	Gly
Lys	Met	Ala
165	170	

&lt;210&gt; 57

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 57

1	5	10	15
Gly	Val	Tyr	Thr
Cys	Tyr	Ala	Met
20	25	30	
Ser	Val	Glu	Leu
Lys	Val	Tyr	Asn
35	40	45	
Thr	Leu	Asn	Thr
Ala	Tyr	Thr	Thr
50	55	60	
Val	Leu	Val	Ile
65	70	75	80
Arg	Gly	Val	Glu
Lys	Pro	Ser	Ser
85	90	95	
Ser	Met	Leu	Ser
Thr	Thr	Pro	Asn
100	105	110	
Lys	Asp	Asp	Gly
Phe	Asp	Arg	Arg
115	120	125	
Pro	Gly	Gln	Gly
Gln	Asn	Gly	Lys
130	135	140	
Val	Pro	Glu	Ala
145	150	155	160
Ser	Val	Ser	Ser
165	170		

&lt;210&gt; 58

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 58

1	5	10	15
Met	Glu	Glu	Ile
Asp	Thr	Cys	Ala
Phe	Leu	Leu	Leu
Leu	Ala	Gly	Leu
145	150	155	160

Ala Leu Glu Ala Ser Asp Pro Val Asp Lys Asp Ser Pro Phe Tyr Tyr  
                     20                   25                   30  
 Asp Trp Glu Ser Leu Gln Leu Gly Gly Leu Ile Phe Gly Gly Leu Leu  
                     35                   40                   45  
 Cys Ile Ala Gly Ile Ala Met Ala Leu Ser Gly Lys Cys Lys Cys Arg  
                     50                   55                   60  
 Arg Thr His Lys Pro Ser Ser Leu Pro Gly Lys Ala Thr Pro Leu Ile  
                     65                   70                   75                   80  
 Ile Pro Gly Ser Ala Asn Thr Cys  
                     85

<210> 59  
 <211> 171  
 <212> PRT  
 <213> Mouse

<400> 59  
 Leu Ser Val Val Leu Gly Gly Thr Leu Tyr Ile Gly His Tyr Leu Ala  
                     1                   5                   10                   15  
 Met Tyr Ser Glu Gly Ala Pro Phe Trp Thr Gly Ile Val Ala Met Leu  
                     20                   25                   30  
 Ala Gly Ala Val Ala Phe Leu His Lys Lys Arg Gly Gly Thr Cys Trp  
                     35                   40                   45  
 Ala Leu Met Arg Thr Leu Leu Val Leu Ala Ser Phe Cys Thr Ala Val  
                     50                   55                   60  
 Ala Ala Ile Val Ile Gly Ser Arg Glu Leu Asn Tyr Tyr Trp Tyr Phe  
                     65                   70                   75                   80  
 Leu Gly Asp Asp Val Cys Gln Arg Asp Ser Ser Tyr Gly Trp Ser Thr  
                     85                   90                   95  
 Met Pro Arg Thr Thr Pro Val Pro Glu Glu Ala Asp Arg Ile Ala Leu  
                     100                   105                   110  
 Cys Ile Tyr Tyr Thr Ser Met Leu Lys Thr Leu Leu Met Ser Leu Gln  
                     115                   120                   125  
 Ala Met Leu Leu Gly Ile Trp Val Leu Leu Leu Leu Ala Ser Leu Thr  
                     130                   135                   140  
 Pro Val Cys Val Tyr Ile Trp Lys Arg Phe Phe Thr Lys Ala Glu Thr  
                     145                   150                   155                   160  
 Glu Glu Lys Lys Leu Leu Gly Ala Ala Val Ile  
                     165                   170

<210> 60  
 <211> 318  
 <212> PRT  
 <213> Mouse

<400> 60  
 Met Leu Gln His Thr Ser Leu Val Leu Leu Ala Ser Ile Trp Thr  
                     1                   5                   10                   15  
 Thr Arg His Pro Val Gln Gly Ala Asp Leu Val Gln Asp Leu Ser Ile  
                     20                   25                   30  
 Ser Thr Cys Arg Ile Met Gly Val Ala Leu Val Gly Arg Asn Lys Asn  
                     35                   40                   45  
 Pro Gln Met Asn Phe Thr Glu Ala Asn Glu Ala Cys Lys Met Leu Gly  
                     50                   55                   60  
 Leu Thr Leu Ala Ser Arg Asp Gln Val Glu Ser Ala Gln Lys Ser Gly  
                     65                   70                   75                   80  
 Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Glu Gln Phe Ser Val Ile

85	90	95
Pro Arg Ile Phe Ser Asn Pro Arg Cys Gly Lys Asn Gly Lys Gly Val		
100	105	110
Leu Ile Trp Asn Ala Pro Ser Ser Gln Lys Phe Lys Ala Tyr Cys His		
115	120	125
Asn Ser Ser Asp Thr Trp Val Asn Ser Cys Ile Pro Glu Ile Val Thr		
130	135	140
Thr Phe Tyr Pro Val Leu Asp Thr Gln Thr Pro Ala Thr Glu Phe Ser		
145	150	155
160		
Val Ser Ser Ser Ala Tyr Leu Ala Ser Ser Pro Asp Ser Thr Thr Pro		
165	170	175
Val Ser Ala Thr Thr Arg Ala Pro Pro Leu Thr Ser Met Ala Arg Lys		
180	185	190
Thr Lys Lys Ile Cys Ile Thr Glu Val Tyr Thr Glu Pro Ile Thr Met		
195	200	205
Ala Thr Glu Thr Glu Ala Phe Val Ala Ser Gly Ala Ala Phe Lys Asn		
210	215	220
Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu Leu Val Leu Ala		
225	230	235
240		
Leu Leu Phe Phe Gly Ala Ala Ala Val Leu Ala Val Cys Tyr Val Lys		
245	250	255
Arg Tyr Val Lys Ala Phe Pro Phe Thr Thr Lys Asn Gln Gln Lys Glu		
260	265	270
Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala Asp Asp Val Asn		
275	280	285
Ala Asn Glu Glu Ser Lys Lys Thr Ile Lys Asn Pro Glu Glu Ala Lys		
290	295	300
Ser Pro Pro Lys Thr Thr Val Arg Cys Leu Glu Ala Glu Val		
305	310	315

&lt;210&gt; 61

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 61

Ala His Met Val Trp Ala Asn Leu Ala Val Phe Val Ile Cys Phe Leu		
1	5	10
Pro Leu His Val Val Leu Thr Val Gln Val Ser Leu Asn Leu Asn Thr		
20	25	30
Cys Ala Ala Arg Asp Thr Phe Ser Arg Ala Leu Ser Ile Thr Gly Lys		
35	40	45
Leu Ser Asp Thr Asn Cys Cys Leu Asp Ala Ile Cys Tyr Tyr Tyr Met		
50	55	60
Ala Arg Glu Phe Gln Glu Ala Ser Lys Pro Ala Thr Ser Ser Asn Thr		
65	70	75
80		
Pro His Lys Ser Gln Asp Ser Gln Ile Leu Ser Leu Thr		
85	90	

&lt;210&gt; 62

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 62

Met Ala Gln Leu Ala Arg Ala Thr Arg Ser Pro Leu Ser Trp Leu Leu		
1	5	10
15		

Leu Leu Phe Cys Tyr Ala Leu Arg Lys Ala Gly Gly Asp Ile Arg Val  
     20                25                30  
 Leu Val Pro Tyr Asn Ser Thr Gly Val Leu Gly Gly Ser Thr Thr Leu  
     35                40                45  
 His Cys Ser Leu Thr Ser Asn Glu Asn Val Thr Ile Thr Gln Ile Thr  
     50                55                60  
 Trp Met Lys Lys Asp Ser Gly Gly Ser His Ala Leu Val Ala Val Phe  
     65                70                75                80  
 His Pro Lys Lys Gly Pro Asn Ile Lys Glu Pro Glu Arg Val Lys Phe  
     85                90                95  
 Leu Ala Ala Gln Gln Asp Leu Arg Asn Ala Ser Leu Ala Ile Ser Asn  
     100               105               110  
 Leu Ser Val Glu Asp Glu Gly Ile Tyr Glu Cys Gln Ile Ala Thr Phe  
     115               120               125  
 Pro Arg Gly Ser Arg Ser Thr Asn Ala Trp Leu Lys Val Gln Ala Arg  
     130               135               140  
 Pro Lys Asn Thr Ala Glu Ala Leu Glu Pro Ser Pro Thr Leu Ile Leu  
     145               150               155               160  
 Gln Asp Val Ala Lys Cys Ile Ser Ala Asn Gly His Pro Pro Gly Arg  
     165               170               175  
 Ile Ser Trp Pro Ser Asn Val Asn Gly Ser His Arg Glu Met Lys Glu  
     180               185               190  
 Pro Gly Ser Gln Pro Gly Thr Thr Val Thr Ser Tyr Leu Ser Met  
     195               200               205  
 Val Pro Ser Arg Gln Ala Asp Gly Lys Asn Ile Thr Cys Thr Val Glu  
     210               215               220  
 His Glu Ser Leu Gln Glu Leu Asp Gln Leu Leu Val Thr Leu Ser Gln  
     225               230               235               240  
 Pro Tyr Pro Pro Glu Asn Val Ser Ile Ser Gly Tyr Asp Gly Asn Trp  
     245               250               255  
 Tyr Val Gly Leu Thr Asn Leu Thr Cys Glu Ala His Ser Lys  
     260               265               270  
 Pro Ala Pro Asp Met Ala Gly Tyr Asn Trp Ser Thr Asn Thr Gly Asp  
     275               280               285  
 Phe Pro Asn Ser Val Lys Arg Gln Gly Asn Met Leu Leu Ile Ser Thr  
     290               295               300  
 Val Glu Asp Gly Leu Asn Asn Thr Val Ile Val Cys Glu Val Thr Asn  
     305               310               315               320  
 Ala Leu Gly Ser Gly Gln Gly Gln Val His Ile Ile Val Lys Glu Lys  
     325               330               335  
 Pro Glu Asn Met Gln Gln Asn Thr Arg Leu His Leu Gly Tyr Ile Phe  
     340               345               350  
 Leu Ile Val Phe Val Leu Ala Val Val Ile Ile Ile Ala Ala Leu Tyr  
     355               360               365  
 Thr Ile Arg Arg Cys Arg His Gly Arg Ala Leu Gln Ser Asn Pro Ser  
     370               375               380  
 Glu Arg Glu Asn Val Gln Tyr Ser Ser Val Asn Gly Asp Cys Arg Leu  
     385               390               395               400  
 Asn Met Glu Pro Asn Ser Thr Arg  
     405

&lt;210&gt; 63

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 63

Met Phe Leu Val Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ala His  
 1 5 10 15  
 Ser Thr Ala Gln Leu Ala Gly Leu Pro Leu Pro Leu Gly Gln Gly Pro  
 20 25 30  
 Pro Leu Pro Leu Asn Gln Gly Pro Pro Leu Pro Leu Asn Gln Gly Gln  
 35 40 45  
 Leu Leu Pro Leu Ala Gln Gly Leu Pro Leu Ala Val Ser Pro Ala Leu  
 50 55 60  
 Pro Ser Asn Pro Thr Asp Leu Leu Ala Gly Lys Phe Thr Asp Ala Leu  
 65 70 75 80  
 Ser Gly Gly Leu Leu Ser Gly Gly Leu Leu Gly Ile Leu Glu Asn Ile  
 85 90 95  
 Pro Leu Leu Asp Val Ile Lys Ser Gly Gly Asn Ser Asn Gly Leu  
 100 105 110  
 Val Gly Gly Leu Leu Gly Lys Leu Thr Ser Ser Val Pro Leu Leu Asn  
 115 120 125  
 Asn Ile Leu Asp Ile Lys Ile Thr Asp Pro Gln Leu Leu Glu Leu Gly  
 130 135 140  
 Leu Val Gln Ser Pro Asp Gly His Arg Leu Tyr Val Thr Ile Pro Leu  
 145 150 155 160  
 Gly Leu Thr Leu Asn Val Asn Met Pro Val Val Gly Ser Leu Leu Gln  
 165 170 175  
 Leu Ala Val Lys Leu Asn Ile Thr Ala Glu Val Leu Ala Val Lys Asp  
 180 185 190  
 Asn Gln Gly Arg Ile His Leu Val Leu Gly Asp Cys Thr His Ser Pro  
 195 200 205  
 Gly Ser Leu Lys Ile Ser Leu Leu Asn Gly Val Thr Pro Val Gln Ser  
 210 215 220  
 Phe Leu Asp Asn Leu Thr Gly Ile Leu Thr Lys Val Leu Pro Glu Leu  
 225 230 235 240  
 Ile Gln Gly Lys Val Cys Pro Leu Val Asn Gly Ile Leu Ser Gly Leu  
 245 250 255  
 Asp Val Thr Leu Val His Asn Ile Ala Glu Leu Leu Ile His Gly Leu  
 260 265 270  
 Gln Phe Val Ile Lys Val  
 275

<210> 64  
 <211> 264  
 <212> PRT  
 <213> Mouse

<400> 64  
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 1 5 10 15  
 Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr  
 20 25 30  
 Gln Asp Leu Tyr Asp Asn Pro Val Thr Ala Val Phe Gln His Glu Gly  
 35 40 45  
 Leu Trp Arg Ser Cys Val Gln Gln Ser Ser Gly Phe Thr Glu Cys Arg  
 50 55 60  
 Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg  
 65 70 75 80  
 Ala Leu Met Ile Val Gly Ile Val Leu Gly Val Ile Gly Ile Leu Val  
 85 90 95  
 Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Asp Asp Ser  
 100 105 110

Ala Lys Ala Lys Met Thr Leu Thr Ser Gly Ile Leu Phe Ile Ile Ser  
 115 120 125  
 Gly Ile Cys Ala Ile Ile Gly Val Ser Val Phe Ala Asn Met Leu Val  
 130 135 140  
 Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Ser Gly Met Gly Gly  
 145 150 155 160  
 Met Gly Gly Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala  
 165 170 175  
 Ala Leu Phe Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly  
 180 185 190  
 Val Met Met Cys Ile Ala Cys Arg Gly Leu Thr Pro Asp Asp Ser Asn  
 195 200 205  
 Phe Lys Ala Val Ser Tyr His Ala Ser Gly Gln Asn Val Ala Tyr Arg  
 210 215 220  
 Pro Gly Gly Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Arg Asn  
 225 230 235 240  
 Lys Lys Ile Tyr Asp Gly Gly Ala Arg Thr Glu Asp Asp Glu Gln Ser  
 245 250 255  
 His Pro Thr Lys Tyr Asp Tyr Val  
 260

<210> 65  
 <211> 132  
 <212> PRT  
 <213> Mouse

<400> 65  
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 1 5 10 15  
 Ala Ser Cys Ala Pro Ala Pro Gly Ser Arg Asp Arg Cys Pro Glu Glu  
 20 25 30  
 Gly Gly Pro Arg Cys Leu Arg Val Tyr Ala Gly Leu Ile Gly Thr Val  
 35 40 45  
 Val Thr Pro Asn Tyr Leu Asp Asn Val Ser Ala Arg Val Ala Pro Trp  
 50 55 60  
 Cys Gly Cys Ala Ala Ser Gly Asn Arg Arg Glu Glu Cys Glu Ala Phe  
 65 70 75 80  
 Arg Lys Leu Phe Thr Arg Asn Pro Cys Leu Asp Gly Ala Ile Gln Ala  
 85 90 95  
 Phe Asp Ser Leu Gln Pro Ser Val Leu Gln Asp Gln Thr Ala Gly Cys  
 100 105 110  
 Cys Phe Pro Arg Val Ser Trp Leu Tyr Ala Leu Thr Ala Leu Ala Leu  
 115 120 125  
 Gln Ala Leu Leu  
 130

<210> 66  
 <211> 764  
 <212> DNA  
 <213> Mouse

<400> 66  
 gcagcaccca gcgccaaggcg caccaggcac cgcgacagac ggcaggagca cccatcgacg 60  
 ggcgtactgg agcgagccga gcagagcaga gagaggcgtg cttgaaacccg agaaccacgc 120  
 cggggcggcat cccccggccg ccgcacgcac aggccggcgc ctcccttgcc tccctgtcc 180  
 ccaccggccc cctccggcca gcatgaggct cctggcggcc gcgctgtcc tgctgtcct 240  
 ggcgtgtgc gcctcgccgcg tggacgggtc caagtgtaa tgttcccgaa agggggccaa 300

gatccgcgtac	agcgacgtga	agaagctgga	aatgaagccca	aagtaccac	actgcgagga	360
gaagatggtt	atcgtcacca	ccaagagcat	gtccaggta	cggggccagg	agcaactgcct	420
gcaccctaag	ctgcagagca	ccaaacgc	cattcaagtgg	tacaatgcct	ggaacgagaa	480
gcgcagggtc	taccaagaat	agggtggacg	atcatggaaa	aaaaaaactcc	aggccagttg	540
agagactca	gcagaggact	ttgcagat	aaataaaagc	cctttttt	tcacaagcat	600
aagacaaatt	atatattgt	atgaagctt	tcttaccagg	gtcagttttt	acattttata	660
gctgtgtgt	aaaggcttcc	agatgtgaga	tccagctcgc	ctgcgcacca	gacttcatta	720
caagtggctt	tttgctgggc	ggttggcggg	gggcgggggg	acct		764

&lt;210&gt; 67

&lt;211&gt; 288

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 67

gcggccgc	tgctcctgct	gctgctggcg	ctgtacaccg	cgcgtgtgg	cgggtccaaa	60
tgcaagtgt	cggaaagg	acccaagatc	cgctacagcg	acgtgaagaa	gctggaaatg	120
aagccaaagt	acccgcactg	cgaggagaag	atggtatca	tcaccaccaa	gagcgtgtcc	180
agttacccag	gtcaggagca	ctgcctgcac	cccaagctgc	agagcaccaa	gcgcctcata	240
aagtggtaca	acgcctggaa	cgagaagcgc	agggtctacg	aagaatag		288

&lt;210&gt; 68

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 68

Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala	Arg	Val	
1			5			10				15					
Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys	Ile	Arg	Tyr
							20		25				30		
Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr	Pro	His	Cys	Glu
							35		40			45			
Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val	Ser	Arg	Tyr	Arg	Gly
						50		55			60				
Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln	Ser	Thr	Lys	Arg	Phe	Ile
						65		70			75		80		
Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys	Arg	Arg	Val	Tyr	Glu		
						85		90			95				

&lt;210&gt; 69

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 69

tccaaatgt	agtgttccc	gaaggggccc	aagatccgt	acagcgacgt	gaagaagctg	60
gaaatgaagc	caaagtaccc	acactgcgag	gagaagatgg	ttatcgta	caccaagagc	120
atgtccagg	accggggcca	ggagcactgc	ctgcaccc	agctgcagag	caccaaacgc	180
ttcatcaatg	gttacaatgc	ctggaacgag	aagcgcagg	tctacgaa	atag	234

&lt;210&gt; 70

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 70

Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp  
 1 5 10 15  
 Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys  
 20 25 30  
 Met Val Ile Val Thr Thr Lys Ser Met Ser Arg Tyr Arg Gly Gln Glu  
 35 40 45  
 His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp  
 50 55 60  
 Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu  
 65 70 75

&lt;210&gt; 71

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Human

&lt;400&gt; 71

tccaaatgca agtgctcccg gaagggaccc aagatccgct acagcgacgt gaagaagctg	60
gaaatgaagc caaagtaccc gcactgcgag gagaagatgg ttatcatcac caccaagagc	120
gtgtccaggta accgaggtca ggagcactgc ctgcacccca agctgcagag caccaagcgc	180
ttcatcaagt ggtacaacgc ctgaaacgag aagcgacagg tctacgaaga atag	234

&lt;210&gt; 72

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Human

&lt;400&gt; 72

Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp  
 1 5 10 15  
 Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys  
 20 25 30  
 Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly Gln Glu  
 35 40 45  
 His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp  
 50 55 60  
 Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu  
 65 70 75

&lt;210&gt; 73

&lt;211&gt; 1460

&lt;212&gt; DNA

&lt;213&gt; Pinus radiata

&lt;400&gt; 73

aaaacgttcca tagtttcctt gccaaactgca agcaatacag tacaagagcc agacgatcga	60
atccctgtcaa gtggtctgaa agtgatggaa agcttggaaat ctgaaaaaac tgttacagga	120
tatcgactc gggactccag tggccacttg tccccattaca cttacaatct cagaaagaaa	180
ggacctgagg atgtaattgt aaaggtcatt tactgcggaa tctgccactc tgattttagtt	240
caaatgcgtta atgaaatgga catgtctcat taccatgg tccctggca tgaagtggtg	300
gggattgtaa cagagattgg cagcgaggta aagaaattca aagtggaga gcatgttaggg	360
gttggttgca ttgttgggtc ctgtcgcagt tgccgttaatt gcaatcagag catggAACAA	420
tactgcacca agaggatttg gacctacaat gatgtgaacc atgacggcac acctactcag	480
ggcggttttg caagcagtat ggtggttgat cagatgtttg tggttcaat cccggagaat	540
cttcctctgg aacaagcggc ccctctgtta tgtcaggggg ttacagttt cagcccaatg	600
aagcatttcg ccatgacaga gcccggaaag aaatgtggga tttgggtttt aggaggcgtg	660
gggcacatgg gtgtcaagat tgccaaagcc tttggactcc acgtgacggt tatcagttcg	720

tctgataaaa	agaaagaaga	agccatggaa	gtcctcgccg	ccgatgctta	tcttggtagc	780
aaggatactg	aaaagatgat	ggaagcagca	gagagcctag	attacataat	ggacaccatt	840
ccagttgttc	atcctcttgg	accatatett	gccttctga	agacaaatgg	aaagctagt	900
atgctggcg	ttttccaga	gcgcgttgcac	ttcgtgactc	ctctcttaat	acttggaga	960
aggagcatag	cttggcagc	atggaggaaa	cacaggaaac	tctagattc	1020	
tgtgcagaga	agaaggtatc	atcgatgatt	gaggttgtgg	gcctggacta	catcaacacg	1080
gccatggaaa	ggttggagaa	gaacgatgtc	cgttacagat	ttgtggtgga	tgttgc当地	1140
agcaagttgg	ataatttagtc	tgcaatcaat	caatcagatc	aatgcctgca	tgcaagatga	1200
atagatctgg	actatgtact	taacatggaaa	gggaaattaa	attttttattt	aggaactcga	1260
tactggttt	tgttacttta	gtttagctt	tgtgaggttg	aaacaattca	atgtttttt	1320
taacttgtat	atgtaaagat	caatttctcg	tgacagtaaa	taataatcca	atgtttctg	1380
ccaaatttaat	atatgtattc	gtattttat	atgaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1440
aaaaaaaaaa	aaaaaaaaaa					1460

&lt;210&gt; 74

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Eucalyptus grandis

&lt;400&gt; 74

aaagcaacac	atngaactct	ctctctctct	ctctctctct	cccccccccc	60	
cccttccaa	ccccccccac	atacagacaa	gtagatacgc	gcacacagaa	gaagaaaaga	120
tgggggttcc	aatgcagtca	atgcactag	cgacggttct	ggccgtccta	acgacatggg	180
cgtggagggc	ggtgaactgg	gtgtggctga	ggccgaagag	gctcgagagg	cttctgagac	240
agcaaggct	ctccggcaag	tcctacacct	tcctggtcgg	cgacctcaag	gagaacctgc	300
ggatgctcaa	ggaagccaag	tccaaagccc	tcgccgtctc	cgatgacatc	aagcctcgtc	360
tct						363

## INTERNATIONAL SEARCH REPORT

International application No. <b>PCT/NZ00/00256</b>
--

**A. CLASSIFICATION OF SUBJECT MATTER**

Int. Cl. 7: C12N 15/11

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

SEE ELECTRONIC DATA BASES

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SEE ELECTRONIC DATA BASES

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EMBL, GenBank, PIR, GenePept: Sequence IDs 1, 36, 2, 37, 3, 38, 4, 39, 5, 40

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank Accession No. AL034558 28 July 1999 Whole Sequence w.r.t. Sequence ID 3	1 - 14
X	GenPept Accession No. CAA29045 21 March 1995 Whole Seqence Frame +2 w.r.t. Sequence ID 4	1 - 14
X	GenBank Accession No. AR018857 5 December 1998 & US 5783182 Whole Sequence w.r.t. Seqence ID 5	1 - 14

Further documents are listed in the continuation of Box C     See patent family annex

* Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search <b>28 March 2001</b>	Date of mailing of the international search report <b>29.03.2001</b>
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Name and mailing address of the ISA/AU  AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaaustralia.gov.au Facsimile No. (02) 6285 3929	Authorized officer  <b>CRAIG ALLATT</b> Telephone No : (02) 6283 2414
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## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/NZ00/00256

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenPept Accession No. CAB4Q181 14 December 1999 Whole Sequence w.r.t. Sequence ID 40	1 - 14

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/NZ00/00256

### Box I Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1.  Claims Nos :  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2.  Claims Nos :  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3.  Claims Nos :  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

### Box II Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See Supplemental Box

1.  As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2.  As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.  As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4.  No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
Claims 1 - 14 partially.(See Supplemental Box)

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.  
 No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ00/00256

### Supplemental Box

(To be used when the space in any of Boxes I to VIII is not sufficient)

#### Continuation of Box No: II

In the present application, the feature that all sequences come from "mammalian sources" does not provide a special technical feature. Genes and their expressed proteins from "mammalian sources" have been sequenced. Cells from "mammalian sources" comprise a variety of different animals and cell types. Moreover the applicant has provided no evidence that the nucleotide sequences of the present application, and the peptides they express, form a unique group of protein types. On the contrary, putative peptides derived from the nucleotide sequences of the application have functions assigned on the basis of their similarity to known proteins expressed by a variety of cell types.

The applicant has grouped the polynucleotides of the application into activity categories according to putative functions of the proteins they encode. However, most of the applicants' groupings do not form a homogenous set of proteins either in structure or function. Moreover, it is noted that most of the peptides encoded by the polynucleotides are assigned to more than one activity category.

The ISA considers that each nucleotide/peptide sequence pair (defined in Table 1 pages 8 - 19) comprises one invention and that there are 35 different inventions (the inventions being numbered sequentially).

However, as a service to the applicants, the ISA will search the first five inventions without inviting additional search fees.

Therefore the ISA has searched SEQ IDs 1, 36, 2, 37, 3, 38, 4, 39, 5, and 40.

## **INTERNATIONAL SEARCH REPORT**

### Information on patent family members

International application No.  
PCT/NZ00/00256

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member					
US	5783182	AU	11609/97	CA	2237929	EP	870057
		WO	9718454				